

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Apr 20 15:17:56 2000; MasPar time 5.15 Seconds 600.911 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: Title:

>US-09-150-947-12 (1-239) from US09150947.pep 1763 1 ESQPDPKPDELHKSSKFTGL.....NKMYDSKDVKIEVYLTTKKK 239

Scoring table: PAM 150 Gap 11

Searched: 131253 seqs, 12956647 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Statistics: a-issued 1:5A_COMB 2:5B_COMB 3:PCT9_COMB 4:backfiles1 Mean 30.280; Variance 145.353; scale 0.208

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	·w	2	_	Result
90	90	90	91	94	96	96	96	96	99	99	99	109	110	110	196	196	201	201	375	375	1760	1760	Score
5.1	5.1	5.1	5.2	ა. ა	5.4	5.4	5.4	5.4	5.6	5.6	5.6	6.2		6.2	11.1	11.1	11.4	11.4	21.3	21.3	99.8	99.8	Query Match Length
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12,	UT.	رى د		Sequence 22,	7,	Sequence 7,	ω	Sequence 3,	'n	'n	Sequence 2,	1,	Sequence 11,			Sequence 10,		Sequence 9,	Sequence 4,	Sequence 4,	Sequence 2,	Sequence 2,	Description
Applicati	Applicatio	Applicatio	Applicati	Applicati	Applicatio	Applicatio	Applicatio	Applicatio	Applicatio	Applicatio	Applicatio	Applicatio	Applicati	Applicati	Applicati	Applicati	Applicatio	Applicatio	Applicatio	Applicatio	Applicatio	Applicatio	1 1 1 1 1 1 1 1
3.58e+01			3.07e+01		1.41e+01		1.41e+01					1.78e+00	1.52e+00			4.81e-07	1.93e-07	1.93e-07	9.01e-22	9.01e-22	1.55e-143	1.55e-143	Pred. No.

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TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE 255 AA; 30159 MW; 364503 CN;	I: 255	ISTICS:	INFORMATION FOR SEO ID NO: 2:	TELEFAX: (303) 863-0223	TELECOMMONICATION INFORMATION:	REFERENCE/COCKET NUMBER: 28/9-29	,005	- 🗠	~	\sim	Α,	APPLICATION NUMBER: US/08/446,918A	CURRENT APPLICATION DATA:	Version	IBM PC	Æ	COMPUTER READABLE FORM;	2	×	••	Denver	700 Lincoln Stre	Ross	25	. 12	NVENTION: GENE T	APPLICANT: Elmslie, Robyn F.	ADDITOANT: Dow Store W	TALENC NO. 3/03131			Sequence 2, Application US/08446918A			XXXXXX		US-08-446-918A-2 STANDARD; PRT; 255 AA.

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Patent No. 5935568
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                                                                                                      TELEFAX: (303) 863-02 INFORMATION FOR SEQ ID NO:
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                                                                                                                                              CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: CONNELL, GAIY J.
REGISTRATION NUMBER: 32,0
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                       COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS
SOFTWARE: PatentIn Release
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Dow, Steve W.
APPLICANT: Elmslie, Robyn E.
APPLICANT: Potter, Terence A.
APPLICANT: GENE THERAPY FOR EFFECTOR CELL REGULATION
                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                       MOLECULE TYPE:
ENCE 255 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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TYPE: a
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                                                                                                      (303) 863-9700
(303) 863-0223
R SEQ ID NO: 2:
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30159 MW;
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         99.88;
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         Score 1760; DB 2;
Pred. No. 1.55e-143;
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Pred. No. 1.55e-143;
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                                                                                          SEQUENCE
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GENERAL INFORMATION:
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                         11 DLRKKSELQGTALGNIKQIYYYNEKAKTENKESHDQFLQHTILFKGFFTDHSWYNDLLVD
                                                                                                                                            TELEFAX: (303) 863-022
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                        CLASSIFICATION: 552
ATTORNEY/AGENT INFORMATION:
NAME: Kovarik, Joseph E.
                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                          MOLECULE TYPE: protein JENCE 233 AA; 27137 MW;
                                                                                                                                                                               REGISTRATION NUMBER: 33,005
REFERICE/DOCKET NUMBER: 50
TELECOMMUNICATION IMPORMATION:
TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: DOW, Steve W.
APPLICANT: Elmslie, Robyn E.
TITLE OF INVENTION: GENE THERAPY FOR T CELL REGULATION
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   ELHKSSKFTGL-MENMK-VLYDDNHVSAINVKSIDQFLYFDLIYSIKDTKLGNYDNVRVE
                                                                                                             TYPE: ami
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STATE: Colora
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00 Lincoln Street, Suite 3500
                                                          21.3%;
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                                              Score 375; DB 1;
Pred. No. 9.01e-22;
56; Mismatches 77
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121 EEKKVPINLWLDGKQNTVPLETVKTNKKNVTVQELDLQARRYLQEKYNLYNSDVFDGKVQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Dow, Steve W.
APPLICANT: Elmslie, Robyn E.
APPLICANT: Potter, Terence A.
TITLE OF INVENTION: GENE THEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/08580806 Patent No. 5935568
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                                                                        11 DLRKKSELQGTALGNLKQIYYYNEKAKTENKESHDQFLQHTILFKGFFTDHSWYNDLLVD 70
                                                                                          / Match 21.3%;
Local Similarity 35.0%;
nes 82; Conservative
                                                                                                            TYPE: am...
TOPOLOGY: linear
MOLECULE TYPE: protein
MOLECULE 233 AA; 27137 MW; 2'
                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2879
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                     TELEFAX: (303) 863-02: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                    FDSKDIVDKYKGKKVDLYGAYYGYQC-----AGG--T--PNK-TACMYGGVTLHDNNRLT 120
                                                     ELHKSSKFTGL-MENMK-VLYDDNHVSAINVKSIDQFLYFDLIYSIKDTKLGNYDNVRVE 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EEKKVPINLWLDGKQNTVPLETVKTNKKNVTVQELDLQARRYLQEKYNLYNSDVFDGKVQ 180
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                                                                                                                                                                                                                                                                                                                                              ZIP:
                                                                                                                                                                                                                                                            CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                               CITY: Denver
STATE: Colora
                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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                                                                                                                                                        LENGTH: 233 amino acids
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(303) 863-0223
R SEQ ID NO: 4:
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                                                                                         Score 375; DB 2; Le
Pred. No. 9.01e-22;
56; Mismatches 77;
                                                                                                                               292215 CN;
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                                                                                                                                                                                                                                                                                                                                                                                  Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     233 AA
                                                                                                            Length 233;
                                                                                           Indels 19;
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                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/08876781 Patent No. 5872233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184 TGYIKF-IENENSFWYDMMPAPGDKFDQSKYLMMYNDNKMYDSKDVKIEVYLTT 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Cole, Barry C.
APPLICANT: Atkin, Curtis
APPLICANT: Pole, Ann
APPLICANT: Oliphant, Arno
                                                                                                                                                                                                                                                                                                                                         TELEFAX: (801)566-075 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: M. Wayne Western
REGISTRATION NUMBER: 22,788
REFERENCE/DOCKET NUMBER: T676
TELECOMMUNICATION INFORMATION:
TELEPHONE: (801)566-6633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Diskette, 3.5 inch, COMPUTER: AST ADVANTAGE NB-SX20 OPERATING SYSTEM: DOS 5.00 SOFTWARE: Word Perfect 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                             MOLECULE TYPE: peptide FRAGMENT TYPE: interna ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 84070
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Mycoplas
TITLE OF INVENTION: Mitogen
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Thorpe, No. 58
                  PUBLICATION INFORMATION:
                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                         STRAIN: S6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RGLIVFHTSTEPSVNYDLFGAQGQ-YSNT-LLRIYRDNKTINSENMHIDIYLYT
                                                                                                       NAME/KEY:
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CLASSIFICATION: 424
                                 IDENTIFICATION METHOD:
                                                                      LOCATION:
                                                                                                                                                                                            ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/876,781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Sandy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
 AUTHORS:
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                                                                                                                                                                               S6
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Jones, C.L.
                                                                                                                                                                                            Staphylococcus aureus
                                                                      residues 39
                                                                                                   staphylococcal enterotoxin B amino acid sequence having sequence similarity to
                                                                                       sequence having MAM.
                                                                                                                                                             unicellular organism
                                                                                                                                                                                                                                 internal fragment
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                                                                      to 65
                                                                                                                                                                                                                                                                                                                                           9.
                                   sequence similarities.
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ORGANISM:

Staphylococcus aureus

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Best Local
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                                                                                                                                                                                                                                                                                                                                                  Sequence 9, Application US/08165038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS: Khai
TITLE: Nucleo
Patent No. 5872233
                                                                                                                                                                                                                                                                                                                             Sequence 9, Application US/08165038 Patent No. 5639869
                                                                                                                                                            ZIP: 84070
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER: DISKette, 3.5 inch, 72
COMPUTER: AST Advantage NB-SX20
OPERATING SYSTEM: DOS 5.00
SOFTWARE: WOR'D PETFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                            Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                           Y Match 11.4%;
Local Similarity 100.0%;
nes 27; Conservative
                                                                  ATTORNEY/AGENT INFORMATION:
NAME: M. Wayne Western
REGISTRATION NUMBER: 22,788
REFERENCE/DOCKET NUMBER: T676
TELECOMMUNICATION INFORMATION:
TELEPHONE: (801)566-6633
                                    TELEFAX: (801)566-0750
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                              APPLICANT: Cole, Barry C.
APPLICANT: Atkin, Curtis L.
APPLICANT: Pole, Ann
APPLICANT: Oliphant, Arnold
TITLE OF INVENTION: Mycoplasma Arthritidis T-Cell
TITLE OF INVENTION: Micogen
NUMBER OF SEQUENCES: 26
                                                                                                                 CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Thorpe, N
 ORIGINAL SOURCE:
        MOLECULE TYPE:
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ISSUE:
PAGES:
                     TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                              APPLICATION NUMBER: US/08/165,038 FILING DATE:
                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                 STREET: 903:
CITY: Sandy
                                                                                                                                                                                                                           STATE:
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27 AA; 3270 MW; 3891 CN;
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                                                                                                                                                                                                                  USA
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              peptide
                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                         22,788
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Pred. No. 1.93e-07;
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE: Nucleo
Patent No. 5639869
TITLE: Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 5872233
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10, Application US/08876781
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IDENTIFICATION METHOD:
PUBLICATION INFORMATION:
AUTHORS: Jones, C.L.
AUTHORS: Khan, S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KSIDQFLYFDLIYSIKDTKLGNYDNVR 27
                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch,
COMPUTER: AST Advantage NB-SX20
OPERATING SYSTEM: DOS 5.00
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: M. Wayne Western
REGISTRATION NUMBER: 22,
                                                            CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Mycopla: TITLE OF INVENTION: Mitogen NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Atkin, Cui
APPLICANT: Pole, Ann
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                                                                                                                                                                                                                                                                            STREET: 9035
CITY: Sandy
STATE: Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL:
VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
NAME/KEY:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                             COUNTRY: US
ZIP: 84070
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DATE: APR-1986
NCE 27 AA; 3270 MW; 3891 CN;
                                                  FILING DATE:
                                                                                                                 FILING DATE:
                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                           ADDRESSEE: Thorpe, No. STREET: 9035 South 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CELL TYPE: unicellular organism
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISSUE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 11.4%;
Similarity 100.0%;
27; Conservative
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                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cole, Barry C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Bacteriol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Curtis L.
                                                                                                                                                                                                                                                                                                                                                                                        Mycoplasma Arthritidis T-Cell
                                                                                                                                US/08/876,781
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Pred. No. 1.93e-07;
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Best Local
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                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                         XXXXXX
                                                                                                                                                                                                                                                                                                                                                  TITLE: Nucleotide Sequence of the Enterotoxin Patent No. 5872233
                                                                                                                            Patent No. 5639869
GENERAL INFORMATION:
                                                                                                                                             Sequence 10,
                                                                                                                                                                                                                                                                                                      JOURNAL: J. Bacteriol.

VOLUME: 166
ISSUE: 1
PAGES: 29-33
DATF:
                                                                                                                                                                                                                                     56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (801)566-0750
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
                                                                                                                                                                                                                                            1 TKLGNYDNYRVEFKNKDLADKYKDKYV 27
                                                                               APPLICANT: Cole, Barry C.
APPLICANT: Atkin, Curtis L.
APPLICANT: Pole, Ann
APPLICANT: Oliphant, Arnold
TITLE OF INVENTION: Mycoplasma Arthritidis T-Cell
TITLE OF INVENTION: Mitogen
                                                                                                                                                                                                                                                                                                                                                                                                                                    CELL T
FEATURE:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch,
COMPUTER: AST Advantage NB-SX20
                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Thorpe, N
                                                                                                                                                                                                                                                                                                                                                                PUBLICATION INFORMATION:
AUTHORS: Jones, C.L.
AUTHORS: Khan, S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
ORGANISM: Sta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide FRAGMENT TYPE: internal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (801)566-6633
                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                     TKLGNYDNVRVEFKNKDLADKYKDKYV
                             STREET: 9035
CITY: Sandy
STATE: Utah
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN: S6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                         ZIP:
                                                                                                                                                                                                                                                                                                                                                                                      IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                 h 11.1%;
Similarity 100.0%;
27; Conservative
                                                                                                                                                                                                                                                                                                : APR-1986
27 AA; 3265 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: unicellular organism
                        84070
                                                                                                                                      ), Application US/08165038 
5639869
                                                     E: Thorpe, No. 5639869th & Western 9035 South 700 East, Suite 200
                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                            staphylococcal enterotoxin B amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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                                                                                                                                                                                                                                                                                                                                                                                                      residues 56 to 82
                                                                                                                                                                                                                                                                                                                                                                                                                    sequence having sequence similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus aureus
                                                                                                                                                                                                       STANDARD;
                                                                            26
                                                                                                                                                                                                                                                                                                 4119 CN;
                                                                                                                                                                                                                                                                 Score 196; DB 2; Le
Pred. No. 4.81e-07;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                       computer searching for sequence similarities.
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        Kb storage
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                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                         TITLE: Nucleo
                                                                                                                                            56
                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: pept:
FRAGMENT TYPE: inte:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                          FEATURE:
TITLE OF INVENTION: Mycoplasma Arthritidis T-Cell
                                                                                                                       9
                                                                                                                                                                                                                    JOURNAL:
VOLUME:
ISSUE: 1
PAGES: 2
                                                                                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                             DATE:
                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                  CELL TYPE:
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                                                                                                                                                                                                                                                   TITLE:
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Query Match 11.1%;
Best Local Similarity 100.0%;
Matches 27; Conservative
                                                                                                                                       Sequence 11, Application US/08165038
                                                                                    Sequence 11, Application US/08165038 Patent No. 5639869
GENERAL INFORMATION:
APPLICANT: Cole, Barry C.
APPLICANT: Atkin, Curtis L.
APPLICANT: Pole, Ann
APPLICANT: Oliphant, Arnold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (801)566-075
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IDENTIFICATION METHOD: compu-
IDENTIFICATION METHOD: seque
PUBLICATION INFORMATION:
AUTHORS: Jones, C.L.
AUTHORS: Khan, S.A.
TITLE: Nucleotide Sequence o
                                                                                                                                                                                                                                                                                                                          1 TKLGNYDNYRVEFKNKDLADKYKDKYV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER

APPLICATION NUMBER

FILTER
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TELECOMMUNICATION INFORMATION:
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LENGTH: 27 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: M. Wayne Western
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                                                                                                                                                                                                                                                                                                     TKLGNYDNVRVEFKNKDLADKYKDKYV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/165,038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene from Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                              AA; 3265 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (801)566-6633
(801)566-0750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence having sequence MAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      staphylococcal enterotoxin B amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                              4119 CN;
                                                                                                                                                                                                                                                                                                                                                                            Pred.
                                                                                                                                                                                                                                                                                                                                                                                           Score 196; DB 1;
Pred. No. 4.81e-07;
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RESULT
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Best Local Similarity 61.5%;
Matches 16; Conservative
                                  XXXXXX
                                                        US-08-876-781-11
                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 22,788
REFERENCE/DOCKET NUMBER: T6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (801)566-6633
TELEPAX: (801)566-0750
INFORMATION FOR SEQ ID NO: 11:
                                                                                                 1 DHYVSATKVKSVDKFLAHDLIYNISD 26
|: ||| :|||:| || ||||:| |
30 DNHVSAINVKSIDQFLYFDLIYSIKD 55
                                                                                                                                                                                         VOLUME: 200
VOLUME: 200
PAGES: 15-20
PATE: 1987
PATE: 1987
                                                                                                                                                                                                                                                                                                  LOCATION: residues 30 to 56 IDENTIFICATION METHOD: compu IDENTIFICATION METHOD: seque PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     CELL TYPE: unicellular organism
FEATURE:
NAME/KEY: staphylococcal enterotoxin C1 amino acid
NAME/KEY: sequence having sequence similarity to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Diskette, 3.5 inch, COMPUTER: AST Advantage NB-SX20 OPERATING SYSTEM: DOS 5.00 SOFTMARE: Word Perfect 5.1 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE: ORGANISM: Sta
                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide FRAGMENT TYPE: internal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 9035
CITY: Sandy
STATE: Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
TYPE: a
                                                                                                                                                                                                                                           AUTHORS: Schlievert, P.M.
TITLE: Nucleotide sequence of the staphylococcal
TITLE: enterotoxin C1 gene and relatedness to
TITLE: other pyrogenic exotoxins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/165,038 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                          AUTHORS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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                                                                                                                                                                                         AA; 3107 MW; 4022 CN;
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9035 South 700 East,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                MAM
                                                                                                                                                                                                                                    Gen. Genet.
                                                        STANDARD;
                                                                                                                                           Score 110; DB 1;
Pred. No. 1.52e+00;
4; Mismatches 6
                                                                                                                                                                                                                                                                                                              sequence
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Query Match
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Matches 1
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                                                                  SEQUENCE
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                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: P
FRAGMENT TYPE: 1
ORIGINAL SOURCE:
ORGANISM: Stap
                                                                                                                                                                                                                                                                                      CELL TYPE: unicellular organism
FEATURE:
NAME/KEY: staphylococcal enterot
NAME/KEY: sequence having sequen
NAME/KEY: MAM.
                                                                                                                                                                                                             PUBLICATION INFORMATION: AUTHORS: Bohach, G.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: T6
TELECOMMUNICATION INFORMATION:
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NAME: M. Wayne Western
REGISTRATION NUMBER: 22,
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Word Perfect 5.1 CURRENT APPLICATION DATA:
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APPLICANT: Atkin, Cur
APPLICANT: Pole, Ann
APPLICANT: Oliphant,
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                                                                                                                                              TITLE:
TITLE:
TITLE:
                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
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CITY: Sandy
                                                                                  PAGES: 15-20
DATE: 1987
                                                                                                           JOURNAL: MO
VOLUME: 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER:
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                                                                                                                                                                                              AUTHORS:
                                                                                                                                                                                                                                           IDENTIFICATION METHOD: IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                            LOCATION:
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    16;
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                                                                27 AA; 3107 MW; 4022 CN;
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 6.2%;
llarity 61.5%;
Conservative
                                                                                                                            Nucleotide sequence of the staphylococcal enterotoxin C1 gene and relatedness to other pyrogenic exotoxins

L: Mol. Gen. Genet.
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9035 South 700 East,
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Atkin, Curtis L.
                                                                                                                                                                                              Schlievert, P.M.
                                                                                                                                                                                                                                                                            residues 30 to 56
                                                                                                                                                                                                                                                                                           staphylococcal enterotoxin C1 amino acid sequence having sequence similarity to MAM.
                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus aureus
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AST Advantage NB-SX20
SYSTEM: DOS 5.00
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                                                                                                                                                                                                                                                                                                                                                                                                        internal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                       peptide
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                  Score 110; DB 2;
Pred. No. 1.52e+00;
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                                                                                                                                                                                                                                           sequence similarities
                                                                                                                                                                                                                                                           computer searching for
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    Mismatches
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    6; Indels
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 RESULT 12
ID US-08-261-825-2
                                                                                                                                                                             Query Match 6.2%;
Best Local Similarity 28.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08946528 Patent No. 5958746
                                                       185 GYIK-FIENENSFWYDMMPAPGD 206
                                                                                                                                    192 LQLIRAI-LKVPEDPTQCFLLFANQTEKDIILREDLEELQARYPNRFKLWFTLDHPPKDW 250
                                                                               251 AYSKGFVTADM-IR-EHLPAPGD 271
                                                                                                          126 LDKYRSITVRVFEDGKN-LLSFDVQTNKKKVTAQELDYLTRHYLVKNKKLYEFNNSPYET 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30 DNHVSAINVKSIDQFLYFDLIYSIKD
                                                                                                                                                                                                                                                               TYPE: amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: line:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                     IMMEDIATE SOURCE:
LIBRARY: PROSNOT16
CLONE: 1709102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/94 FILING DATE: Filed Herewith PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: COrley, Neil C.
TITLE OF INVENTION: ELECTRON TRANSPORT PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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                                                                                                                                                                                                                        305 AA; 34095 MW; 500339 CN;
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                                                                                                                                                                  Conservative
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 STANDARD;
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                                                                                                                                                               Score 109; DB 2;
Pred. No. 1.78e+00;
25; Mismatches 29
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 174 AA.
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                                                                                                                                                                                            Length 305;
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                                       Sequence
                                                                                                                          PCT-US95-07748A-2
Sequence 2, Application PC/TUS9507748A GENERAL INFORMATION:
                                                                                                                                                                                                124 DYLIQLDSDKIDYAEKYGEKARENFEESY 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08261825 Patent No. 5558993
                                                                                                                                                                                                                                                                                       / Match 5.6%;
Local Similarity 29.2%;
nes 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (619) 455-51 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                               62 DN-VRVEFKNKDLADKYKDKYVDVFGANY
                                                                                                                                                                                                                                                             65 AKAPEIRGSLRKIGIKEN-SVLLDALDVVGFIKSKITTDFLSFIIMNINSLIKGYPNSIF 123
                                                                                                                                                                                                                                  6 PKPDELHKSSKFTGLMENMKVLYDD-NHVSAINVKSIDQFL-YFDL-IYS-IKDTKLGNY 61
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: TUMARKIN, LISA A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: CLONED Borrelia burgdorferi VIRULENCE TITLE OF INVENTION: PROTEIN
                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein 
ENCE 174 AA; 20290 MW; 153533 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/0 FILING DATE: 17-JUN-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: P-
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 90067
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                                       Application PC/TUS9507748A
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1880 Century Park East, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                  174 amino acids
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Haake, David A.
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                                                                                                                          STANDARD;
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Pred. No. 8
25; Mismat
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Mismatches 32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: HAILE, Ph.D., LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 0741
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
TELEPHONE: (619) 678-5099
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                            124 DYLIQLDSDKIDYAEKYGEKARENFEESY 152
                                                                                                                                                                       Sequence 2, Application US/08719124 Patent No. 5854395
                                                         GENERAL INFORMATION:
APPLICANT: Champion, Cheryl I.
APPLICANT: Lovett, Michael A.
APPLICANT: Haake, David A.
APPLICANT: Miller, James N.
APPLICANT: Miller, James N.
APPLICANT: Blanco, David R.
TITLE OF INVENTION: CLONED Borrelia burgdorferi VIRULENCE
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity nes 26; Conser
                                                                                                                                                                                                                                                                                                                                     62 DN-VRVEFKNKDLADKYKDKYVDVFGANY 89
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein JENCE 174 AA; 20290 MW; 153533 CN;
                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: The Regents of the University of California TITLE OF INVENTION: CLONED Borrelia burgdorferi VIRULENCE
                                                                                                                                                                                                                                                                                                                                                                                    PKPDELHKSSKFTGLMENMKVLYDD-NHVSAINVKSIDQFL-YFDL-IYS-IKDTKLGNY 61
STREET:
CITY: L
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: ami
TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
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                                   ADDRESSEE:
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           Los Angeles
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                     1880 Century Park East, Suite 500
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                                   Spensley Horn Jubas & Lubitz
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                                                                                                                                                                                                                                                                                    STANDARD;
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                                                                                                                                                                                                                                              Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                    124 DYLIQLDSDKIDYAEKYGEKARENFEESY 152
                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Johnson, Howard M.
APPLICANT: Pontzer, Carol H.
APPLICANT: Griggs, Nathan D.
TITLE OF INVENTION: Superanti
TITLE OF INVENTION: Peptides
                                                                                                                                                                                                                                                                                                                                                                                                         62 DN-VRVEFKNKDLADKYKDKYVDVFGANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 AKAPEIRGSLRKIGIKEN-SVLLDALDVVGFIKSKITTDFLSFIIMNINSLIKGYPNSIF 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (619)
INFORMATION FOR SEQ
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        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                              NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
JENCE 174 AA; 20290 MW; 153533 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: PD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/261,825
FILING DATE: 17-JUN-1994
ATTORNEY_AGENT INFORMATION:
NAME: TUMARKIN, LISA A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          PKPDELHKSSKFTGLMENMKVLYDD-NHVSAINVKSIDQFL-YFDL-IYS-IKOTKLGNY 61
                                                                     COUNTRY: US
                                                                                              CITY: Gainesville
STATE: FL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/719,124 FILING DATE: 24-SEP-1996
                                                                                                                       ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: P-38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 90067
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llarity 29.2%;
Conservative
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                                                                                    USA
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) 455-5110
NO: 2:
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Pred. No. 8.83e+00;
25; Mismatches 32
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           Version
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Length 174;

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GC APPLICATION NUMBER: US/08/220,378

GC CILING DATE: DD: 530

GC PRIOS PARTED: STATE DO: 57941,497

GC PRIOS PARTED: US/07/941,497

GC PRICE DATE: US/07/941,497

GC PRICE SALIVABORINE US/07/941,497

GC REFERENCE/DOCRET NUMBER: 131,794

GC REFERENCE/DOCRET NUMBER: UP16.C1

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

Run on: MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Thu Apr 20 15:16:39 2000; MasPar time 9.82 Seconds 576.551 Million cell updates/sec

Description: Perfect Score: Sequence: >US-09-150-947-12 (1-239) from US09150947.pep 1763 1 ESQPDPKPDELHKSSKFTGL.....NKMVDSKDVKIEVYLTTKKK 239

Searched: 188963 seqs, 23686106 residues Scoring table:

PAM 150 Gap 11

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq36 1:geneseqp

Statistics: Mean 32.417; Variance 153.333; scale 0.211

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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747 746	749	749	751	752	753	753	755	756	756	756	758	760	1107	1135	1176	1176	1725	1725	1760	1763	Score	
42.4	42.5	42.5	42.6	42.7	42.7	42.7	42.8	42.9	42.9	42.9	43.0	43.1	62.8	64.4	66.7	66.7	97.8			100.0	Match L	Query
190 190	221 190	221	190	190	190	190	190	190	190	. 190	190	190	238	238	239	239	239	239	255	239	Length D	
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	Streptococcal pyrogeni Staphylococcus enterot											w	_	_	Н	_	Staphylococcal enterot	Staphylococcal enterot	Staphylococcus enterot	Synthetic SEB protein	Description	
	4.56e-54 6.85e-54	4.56e-54				2.02e-54	1.34e-54	1.09e-54	1.09e-54	1.09e-54	7.29e-55	4.85e-55	5.97e-86	1.86e-88			1.44e-141	1.44e-141	9.88e-145	5.29e-145	Pred. No.	

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726	728	730	732	732	737	738	738	739	739	740	740	740	740	742	742	742	745	745	745	745	746
41.2	41.3	41.4	41.5	41.5	41.8	41.9	41.9	41.9	41.9	42.0	42.0	42.0	42.0	42.1	42.1	42.1	42.3	42.3	42.3	42.3	42.3
190	251	251	251	190	190	251	251	251	190	251	251	251	190	190	190	190	251	190	190	190	190
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R42011	W59781	W12148	W12146	R42013	R42002	W12147	W12154	W59798	R42001	W59780	W12097	W12150	R42004	R42010	R42006	R41999	W12153	R42003	R41997	R41990	R42005
Staphylococcus enterot	Amino acid sequence of	Streptococcus pyogenes	Streptococcus pyogenes	Staphylococcus enterot	Staphylococcus enterot	Streptococcus pyogenes	Streptococcus pyogenes	Amino acid sequence of	Staphylococcus enterot	Amino acid sequence of	Streptococcus pyogenes	Streptococcus pyogenes	Staphylococcus enterot		Staphylococcus enterot	Staphylococcus enterot	Streptococcus pyogenes	Staphylococcus enterot	Staphylococcus enterot	Staphylococcus enterot	Staphylococcus enterot
4.92e-52	3.27e-52	2.18e-52	1.45e-52	1.45e-52	5.24e-53	4.28e-53	4.28e-53	3.49e-53	3.49e-53	2.85e-53	2.85e-53	2.85e-53	2.85e-53	1.90e-53	1.90e-53	1.90e-53	1.03e-53	1.03e-53	1.03e-53	1.03e-53	8.39e-54

ALIGNMENTS

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Query Match Best Local Matches 2	w64647 s w64647; 23-OCT-1 Syntheti Enteroto toxic sh therapeu Syntheti Staphylo W0982944 -09-70-71 30-DEC-1 30-DEC-1 30-DEC-1 30-DEC-1 1 staphylo W01; 98- WPI; 98- OF O	TT
Query Match 100.0%; Best Local Similarity 100.0%; Matches 239; Conservative	W64647 standard; peptide; 239 AA. W64647; W64647; 23-OCT-1998 (first entry) Synthetic SEB protein fragment. Enterotoxin B; SEB; pyrogenic exotoxin; PPT; proxic shock; toxin-mediated activation; T-cell therapeutic; vaccine; food poisoning. Synthetic. Staphylococcus aureus. W09829444-A1. 30-DEC-1996; II-119938. (YISS) YISSUM RES & DEV CO. Arad G, Kaempfer R; WPI; 98-388042/33. 30-DEC-1996; iI-119938. (YISS) YISSUM RES & DEV CO. Arad G, Kaempfer R; WPI; 98-388042/33. New peptide(s) derived from pyrogenic exotoxin natagonising toxin-mediated activation of Toxin treatment of toxic shock caused by exotoxin(s) Example 8; Page 41; 68pp; English. W64636-W64657 are peptides homologous to the armound of a pyrogenic exotoxin (PET), and deicapable of eliciting protective immunity again: Example 8; Page 41; 68pp; English. W64636-W64657 are peptides homologous to the armagenising toxin-mediated activation of Toxin (PET) or by a mixture of PETs. Such peptides and tragenising toxin-mediated activation of Toxin (PET) induced mRNA encoded by TNF-beta genes. The peptides may be used to provoccines for the treatment of prophylaxis of the first genes. The peptides may be used to provoccines for the treatment of prophylaxis of the peptides can also be used for the treatment (especially food poisoning) and toxic shock can the peptides can also be used for alleviating sequence 239 AA;	1
ıilari: Con:	less (first control of a process of a proces	
100.0% larity 100.0% Conservative	rd; peptide; (first entry) protein frag; (SEB; pyroget toxin-mediate vaccine; food s aureus. IL10438. IL-119938. M RES & DEV C fer R; 2/33.) derived fro toxin-mediate toxic shock c ge 41; 68pp; are peptides pyrogenic ex iciting prote ixture of pert toxin-mediate toxin mediate toxin mediate toxin mediate sprogenic ex iciting prote ixture of pert toxin-mediate toxin mediate toxin prote ixture of pert toxin mediate toxin mediate toxin mediate toxin mediate of pert toxin mediate	
100.0%; 100.0%; vative	yfirst entry) protein fragment SEB; pyrogenic coxin-mediated ac raccine; food poi. aureus. L1-11998. L1-11998. GRES; DEV CO. FOR RES; ADEV CO. FOR RES;	
Score Pred. 0;	y) agment. genic exotos ted activati od poisoning co. co. co. co. co. co. co. co.	
Score 1763; DB 1; Pred. No. 5.29e-145; 0; Mismatches 0;	ing. ing. ing. y enic eation y exot y exot y (PET) mmunil mention ation	
DB 5.29e- ches	PET; T-ce pxotox	
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DB 1; Length 239; !9e-145; les 0; Indels	W64647; w646467; w64647;	
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                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PT Recombinant molecule encoding super:antigen and opt. cytokine or PT chemokine - controls activity of effector cells (T cells, monocytes, PT natural killer cells), used for gene therapy of cancer PS Example 1; Page 96-97; 131pp; English.

CC (W06737) superantigen. Nucleic acids encoding superantigens (see CC (W06737) superantigen. Nucleic acids encoding superantigens (see CC also W06738-39), esp. truncated forms of the superantigen lacking CC infectious diseases and immunological disorders. The nucleic acid, Optionally in combination with cytokine or chemokine nucleic acids, CC is delivered to an animal using e.g. liposomes. It acts by CC controlling the activity of effector cells, such as T-cells, CC macrophages, monocytes and/or natural killer cells. Localised CC prodn. of an effective but non-toxic amount of encoded proteins and controlling the activity but non-toxic amount of encoded proteins
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Best Local S
Matches 23
   Staphylococcal
                            R13206 standard; Protein; (239 AA)
R13206;
15-OCT-1991 (first entry)
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18-MAY-1995; US-446918.
18-MAY-1995; US-580806.
29-DEC-1995; US-580806.
(NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY MED.
DOW SW, Elmslie RE, Potter TA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus sp.
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lymphocyte; monocyte; natural killer cell; gene therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus enterotoxin B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 99.8%;
Local Similarity 99.6%;
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97-011857/01.
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                                                                                                                                                                                                                                             PYETGYIKFIENENSFWYDMMFAPGDKFDQSKYLMMYNDNKMVDSKDVKIEVYLTTKKK 255
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   enterotoxin B
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Pred. No. 9.88e-145;
1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Treating cancer with enterotoxin from Staphylococcus aureus administered by IV injection, having same tumoricidal activity as Staphylococcal protein A without potential toxic reactions as Staphylococcal protein A without potential toxic reactions placed some protein A without potential toxic reactions placed and purified from Saureus. It can be used for treating cancer, activating cytokine mediators and procoagulant systems, augmenting natural killer cell cytotoxicity, etc. The enterotoxin can be administered intravenously, optionally with buprofen to attenuate toxic reaction to SEB. Synthetic polypeptides having structural homology to Staphylococcal exotoxins are claimed, provided the homology includes statistically significant sequence homology, alignment of Cysteine residues and similar hydronathy profiles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R45014 standard; protein; (239 AA R45014; 08-JUN-1994 (first entry)
                                  Disclosure; Fig 1; 90pp; English.
The sequences given in R45011-21 are Staphylococcal enterotoxins which may be used in the methods of the invention for treating call in a patient. These SEs, and homologues of them, can be used as tumouricidal agents for treating cancers and autoimmune disease. They exhibit tumouricidal activity and toxicity identical to that They exhibit tumouricidal activity and toxicity identical to that observed for the Protein A perfusion system. They may be administ
                                                                                                                                                                                                                                                                                                                                                   WPI; 93-405418/50.
Use of staphylococcal enterotoxin(s) and homologues - use of staphylococcal enterotoxin or the treatment of the treatment o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1993; U05213.
01-JUN-1992; US-891718
(STON/) STONE J L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similar hydropathy profiles.
See R13203-R13211.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (STON/) STONE J L.
(TERM/) TERMAN D S.
Stone JL, Terman D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcal
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Pred. No. 1.44e-141;
3; Mismatches 2;
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The sequences given in R45011-21 are Staphylococcal enterotoxins which may be used in the methods of the invention for treating ca in a patient. These SEs, and homologues of them, can be used as tumouricidal agents for treating cancers and autoimmune disease. They exhibit tumouricidal activity and toxicity identical to that observed for the Protein A perfusion system. They may be administ by i.v. injection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Use of staphylococcal enterotoxin(s) and homologues - for treating cancer in a patient or for the treatment of auto-immune
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01-JUN-1992;
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Best Local S
Matches 16
                                                                                                              Staphylococcus aureus. W09324136-A. 09-DEC-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treating cancer, activating cytokine mediators and procoagulant systems, augmenting natural killer cell cytotoxicity, etc. The enterotoxin can be administered intravenously, optionally with ibuprofen to attenuate toxic reaction to SEC1. Synthetic polypeptides having structural homology to Staphylococcal exotoxins are claimed, provided the homology includes statistically significant sequence homology, alignment of Cysteine residues and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treating cancer with enterotoxin from Staphylococcus aureus administered by IV injection, having same tumoricidal activity as Staphylococcal protein A without potential toxic reactions Disclosure; Fig 1; 74pp; English.

SECI was isolated and purified from S.aureus. It can be used for the state of the st
   (STON/)
                                                          01-JUN-1993; U05213.
01-JUN-1992; US-891718
                                                                                                                                                                                                       Staphylococcal enterotoxin SEC3. Staphylococcal enterotoxin; SE; autoimmune disease; toxicity; Pr
                                                                                                                                                                                                                                                                                          R45016;
08-JUN-1994
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17-JAN-1990; US-466577.
(TERM/) TERMAN D S.
Terman DS;
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R13203-R13211.
uence 239 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ESQPDPTPDELHKASKFTGLMENMKVLYDDHYVSATKVKSVDKFLAHDLIYNISDKKLKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ≍ ..
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                                                                                                                                                                                                                                                                                                                                                       6 standard; protein; 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HNGNQLDK-Y-RSITVRVFEDGKNLLSFDVQTNKKKVTAQELDYLTRHYLVKNKKLYEFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YDNVRVEFKNKDLADKYKDKYVDVFGANYYYQCYFSKKTNDINSHETDKRKTCMYGGVTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l Similarity
160; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lococcus aureus.
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   STONE J L.
TERMAN D S.
                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66.78;
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Pred.
41; M
                                                                                                                                                                                                             Protein A; perfusion system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B
                                                                                                                                                                                                                                         cancer; tumouricidal agent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e 1176; DB 1,
1. No. 3.93e-92;
1. No. 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tumouricide
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Best Local S
Matches 15
                                                                                                                                                                                                                                                                                                           SEC3 was isolated and purified from S.aureus. It can be used for treating cancer, activating cytokine mediators and procoagulant systems, augmenting natural killer cell cytotoxicity, etc. The enterotoxin can be administered intravenously, optionally with lbuprofen to attenuate toxic reaction to SEC3. Synthetic polypeptides having structural homology to Staphylococcal exotoxins are claimed, provided the homology includes statistically significant sequence homology, alignment of Cysteine residues and significant sequence homology, alignment of Cysteine residues
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The sequences given in R45011-21 are Staphylococcal enterotoxins which may be used in the methods of the invention for treating cain a patient. These SEs, and homologues of them, can be used as tumouricidal agents for treating cancers and autoimmune disease. They exhibit tumouricidal activity and toxicity identical to that observed for the Protein A perfusion system. They may be administly injection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEC3;
                                                                                                                                                                                                                                      similar hydropathy profiles.
See R13203-R13211.
Sequence 238 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Treating cancer with enterotoxin from Staphylococcus aureus administered by IV injection, having same tumoricidal activity as Staphylococcal protein A without potential toxic reactions bisclosure; Fig 1, 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TERM/) TERMAN D S. Terman DS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-JAN-1991; U00342.
17-JAN-1990; US-466577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9110680-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcal enterotoxin C3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-OCT-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R13208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R13208 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPYETGY IKFIENE - NSFWYDMMPAPGDKFDQSKYLMMYNDNKMVDSKDVKIEVYLTTKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e JL, Terman
93-405418/50
                                SQPDPTPDELHKSSEFTGTMGNMKYLYDDHYVSATKVMSVDKFLAHDLIYNISDKKLKNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPYETGYIKFIENNGNTFWYDLMPAPGDKFDQSKYLMMYNDNKTVDSKSVKIEVHLTTKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNVRVEFKNKDLADKYKDKYVDVFGANYYYQCYFSKKTNDINSHETDKRKTCMYGGVTEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DKVKTELLNEDLAKKYKDEVVDVYGSNYYVNCYFSSK-DNV-GKVTGG-KTCMYGGITKH 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SQPDPTPDELHKSSEFTGTMGNMKYLYDDHYVSATKVMSVDKFLAHDLIYNISDKKLKNY
        SQPDPKPDELHKSSKFTGLMENMKVLYDDNHVSAINVKSIDQFLYFDLIYSIKDTKLGNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer treatment;
                                                                                                                    l Similarity
155; Conse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . Similarity
156; Conse
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                                                                                                                 62.8%;
llarity 64.6%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pyrogen;
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Pred. No. 1.86e-88;
41; Mismatches 37;
                                                                                                                    Score
Pred.
39; M
                                                                                                                 re 1107; DB 1;
d. No. 5.97e-86;
Mismatches 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for
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                                                                                                                    40;
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                                                                                                                    Gaps
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents the Staphylococcus enterotoxin B (SEB) super antigen (SAg). Mutant versions of this sequence generated by random mutation by PCR, may be used to modify the T-cell response. elicited by an antigen, by interacting with specific Vbeta elements of the T-cell receptors. This T-cell response modulation may be useful in a wide variety of autoimmune diseases, where self-reactive T-cells may be activated by SAg that bind to particular Vbeta types. Sequence 190 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Preventing or treating toxic effects of super antigens - by adm new modified or mutated super antigen which induces antibodies not T-cell activation Disclosure; Fig 3; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R41989 standard; protein; 190
R41989;
21-APR-1994 (first entry)
Staphylococcus enterotoxin B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-JAN-1992; US-827540.
(NAJE-) NAT JEWISH CENT
Kappler JW, Marrack P;
WPI; 93-320314/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-AUG-1993.
28-JAN-1993; U00839
28-JAN-1992; US-827
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162. .:
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59.5%;
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Pred. No. 4.85e-55;
29; Mismatches 48
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R42007 standard; protein; 190 R42007; 21-APR-1994 (first entry)

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Best Local S
Matches 11
WO9314634-A.
05-AUG-1993.
28-JAN-1993. U00839.
28-JAN-1992. US-827540.
(NAJE-) NAT JEWISH CENT I
KAPPLE JW. MATTACK P;
WPI: 93-320314/40.
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28-JAN-1993, U00839,
28-JAN-1992, US-827540,
(NAJE-) NAT JEWISH CENT 1
KAPPLET JW, MARTACK P;
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Disclosure; Fig 3; 54pp; English.

The sequences given in R41990-2013 are mutant versions of the Staphylococcus enterotoxin B (SEB) super antigen (SAg). These mutants generated by random mutation by PCR, may be used to modify the T-cell response elicited by an antigen, by Interacting with specific Vbeta elements of the T-cell receptors. This T-cell response modulation may be useful in a wide variety of autoimmune diseases, where self-reactive T-cells may be activated by SAg that bind to particular
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21-APR-1994
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97. .157
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162. .1
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d super antigen which in
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                                             IMMUNOLOGY & RESPIRATORY
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No. 7.29e-55;
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28-JAN.1993; U00839.
28-JAN.1992; US-877540.
(NAJE-) NAT JEWISH CENT 1
(NAJE-) NAT JEWISH CENT 1
KAPPLET JW. MATRACK P;
                                                                                                                                new modified or mutated super antigen which induces antibodies but not T-cell activation pisclosure; Fig 3; 54pp; English.

The sequences given in R41990-2013 are mutant versions of the Staphylococcus enterotoxin B (SEB) super antigen (SAg). These mutants generated by random mutation by PCR, may be used to modify the T-cell response elicited by an antigen, by interacting with specific vbeta elements of the T-cell receptors. This T-cell response modulation may be useful in a wide variety of autoimmune diseases, where self-reactive T-cells may be activated by SAg that bind to particular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus enterotoxin B mutant BR-291. Staphylococcus; enterotoxin B; SEB; super antigen; random mutation; PCR; modify; T-cell; response; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R41993 standard; protein;
R41993;
21-APR-1994 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     autoimmune disease.
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Staphylococcus; enterotoxin B; SEB; super antigen; SAg; receptor; random mutation; PCR; modify; T-cell; response; antigen; Vbeta el
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(NAJE-) NAT JEWISH CENT
Kappler JW, Marrack P;
WPI; 93-320314/40.
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05-AUG-1993.
28-JAN-1993; U00839
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21-APR-1994 (first entry)
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97. .157
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Pred. No. 1.09e-54;
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28-JAN-1993; U00839.

28-JAN-1992; US-827540.

(NAJE-) NAT JEWISH CENT I

Kappler JW, Marrack P;

WPI; 93-320314/40.
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05-AUG-1993.
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Disclosure; Fig 3; 54pp; English.

The sequences given in R41990-2013 are mutant versions of the Staphylococcus enterotoxin B (SEB) super antigen (SAg). These mutants generated by random mutation by PCR, may be used to modify the T-cell response elicited by an antigen, by interacting with specific Vbeta elements of the T-cell receptors. This T-cell response modulation may be useful in a wide variety of autoimmune diseases, where self-vect tree T-cells may be activated by SAg that bind to particular
                                                                                                                                                                                                                                                                                                                                     Staphylococcus enterotoxin B mutant BA-15.
Staphylococcus; enterotoxin B; SEB; super antigen; SAg; receptor; random mutation; PCR; modify; T-cell; response; antigen; Vbeta el
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Staphylococcus; enterotoxin B; SEB; super antigen; SAg; receptor; random mutation; PCR; modify; T-cell; response; antigen; Vbeta element;
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Best Local Similarity 58.9%;
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1. Staphylococcus enterotoxin B (SEB) super antigen (SAg). These mutants generated by random mutation by PCR, may be used to modify the T-cell response elicited by an antigen, by interacting with specific Vbeta elements of the T-cell receptors. This T-cell response modulation may be useful in a wide variety of autoimmune diseases, where self-reactive T-cells may be activated by SAg that bind to particular volucta types.
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28-JAN-1992; US-827540.
28-JAN-1992; US-827540.
(NAJE:) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.
Kappler JW, Marrack P,
WPI; 93-320314/40.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Thu Apr 20 15:08:07 2000; MasPar time 15.27 Seconds 467.552 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Title: >US-09-150-947-12 (1-239) from US09150947.pep 1763 1 ESQPDPKPDELHKSSKFTGL.....

ESQPDPKPDELHKSSKFTGL.....NKMVDSKDVKIEVYLTTKKK 239

Scoring table: PAM 150 Gap 11

Searched: 82229 seqs, 29864866 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot38 1:swissprot

Statistics: Mean 47.318; Variance 95.221; scale 0.497

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

45	44	43	42	41	40	39	38	37	36	<u>3</u> 5	34	ω _.	32	31	30	29	28	27	26	25	24
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MEROZOITE SURFACE PROT	GLUCOSYLTRANSFERASE-I	DNA POLYMERASE I (EC 2	NAM7 PROTEIN (NONSENSE	PROTEIN-TYROSINE PHOSP	HYPOTHETICAL 63.9 KD P	CYTOCHROME P450 52A11	CYTOCHROME P450 52A10	PROBABLE GLUTAMYL-TRNA	PROTEIN-TYROSINE PHOSP	CYSTIC FIBROSIS TRANSM	PROTEIN 01.	PROTEIN-TYROSINE PHOSP	NUCLEAR PORE COMPLEX P	PHENYLALANINE AMMONIA-	ATP-DEPENDENT DNA HELI	EARLY TRANSCRIPTION FA	PUTATIVE TYROSINE 3-MO	ENCAPSIDATION PROTEIN	SPERMATOCYTE PROTEIN S	PHOSPHOENOLPYRUVATE CA	AEROBIC RESPIRATION CO
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ALIGNMENTS

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MEDILINE: 94203282. JARDETZKY T.S., BROWN J.H., GORGA J.C., STERN L.J., URBAN R.G., CHI Y.I., STAUFFACHER C., STROMINGER J.L., WILEY D.C.; "Three-dimensional structure of a human class II histocompatibility molecule complexed with superantigen."; Nature 368:711-718(1994).	MEDLINE: 93063291. MEDLINE: 93063291. SWAMINATHAN S., FÜREY W.F. JR., PLETCHER J., SAX M.; "Crystal structure of staphylococcal enterotoxin B, a superantigen."; Nature 359:801-806(1992) Y-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF COMPLEX WITH MHC II.	UENCE OF 28-266 (S-6). LINE; 71007902. NG IY., BERGDOLL M.S.; e primary structure of s nogen bromide peptides o and the complete amino Biol. Chem. 245:3518-352	SEQUENCE OF 40-91 FROM N.A. SEQUENCE OF 40-91 FROM N.A. MEDLINE; 85298255. MARKELI D.M., JONES C.L., JOHNS M.B., MUSSEY G.J., KHAN S.A.; RANKELI D.M., JONES C.L., JOHNS M.B., MUSSEY G.J., KHAN S.A.; RANKELI D.M., JONES C.L., JOHNS M.B., MUSSEY G.J., KHAN S.A.; RANKELI D.M., JONES C.L., JOHNS M.B., MUSSEY G.J., KHAN S.A.; RANKELI D.M., KHAN S.A.; BYCO. Natl. Acad. Sci. U.S.A. 82:5850-5854(1985).	SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE: 86168029. JONES C.L., KHAN S.A.; "Nucleotide sequence of the enterotoxin B gene from Staphylococcus aureus."; Al. Bacteriol. 166:29-33(1986).	LT 1 ETXB_STAAU STANDARD; PRT; (266 AA.) p01552; 21-JUL-1986 (Rel. 01, Created) 13-AUG-1987 (Rel. 05, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) ENTEROTOXIN TYPE B PRECURSOR (SEB). ENTB. Staphylococcus aureus. Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Staphylococcus.

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"Crystal structure of microbial superantiges staphylococcal enterotoxin B at 1.5-A resolution: implications for superantiger recognition by MHC class II molecules and T-cell receptors.";

J. MOI. Biol. 277:61-79(1998).

"I DEPSEASE: STAPHYLOCOCCAL ENDEROTOXINS CAUSE THE INTOXICATION STAPHYLOCOCCAL FOOD POISONING SYNDROME.

"STAPHYLOCOCCAL FOOD POISONING SYNDROME."

"STAPHYLOCOCCAL FOOD POISONING SYNDROME."
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LI H., LLERA A., TSUCHIYA D.,
KARJALAINEN K., MARIUZZA R.A.;
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                                                           YDNVRVEFKNKDLADKYKDKYVDVFGANYYYQCYFSKKTNDINSHQTDKRKTCMYGGVTE
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                                                                                                                                                            Score 1760; DB 1;
Pred. No. 0.00e+00;
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                                                                                                                                                                                                          -> EQ (IN REF. 3).
-> N (IN REF. 3).
-> ND (IN REF. 3).
                                                                                                                                                                                                                               Mismatches
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-> ENT (IN REF. 3).
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CONFLICT
SEQUENCE
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01-JAN-1990
15-JUL-1999
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CHAIN
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P01553;
                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 28-266.

MEDLINE; 33213327.

SCHMIDT J.J., SPERO L.;

SCHMIDT J.J., SPERO L.;

The complete amino acid sequence of staphylococcal enterotoxin J. Biol. Chem. 258:6300-6306(1983).

-I- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION STAPHYLOCOCCAL FOOD POISONING SYNDROME.

-I- SIMILARITY: THE DIFFERENT S.AUREUS ENTEROTOXINS AND S.PYOGEN
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                                                                                                                                                                                                                                                                                    Enterotoxin;
                                                                                                                                                                                                                                                                                             PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
PFAM; PF01123; Stap_Strp_toxin; 1.
                                                                                                                                                                                                                                                                                                                                              PIR; A01816; ENSAC1.
PIR; S06356; S06356.
                                                                                                                                                                                                                                                                                                                                                                       EMBL;
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"Nucleotide sequence of the s
relatedness to other pyrogeni
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SSPYETGYIKFIENNGNTFWYDMMPAPGDKFDQSKYLMMYNDNKTVDSKSVKIEVHLTTK
                        HNGNQLDK-Y-RSITVRVFEDGKNLLSFDVQTNKKKVTAQELDYLTRHYLVKNKKLYEFN
                                     HEGNHFDNGNLQNVLIRVYENKRNTISFEVQTDKKSVTAQELDIKARNFLINKKNLYEFN
                                                                                     ESQPDPKPDELHKSSKFTGLMENMKVLYDDNHVSAINVKSIDQFLYFDLIYSIKDTKLGN
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88038352.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ence of the staphylococcal enterotoxin
ther pyrogenic toxins.";
209:15-20(1987).
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27
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                                                                                                                                                                                                                        30546 MW;
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                                                                                                                                                                                   Score 1183;
Pred. No. 1
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FE00255A CRC32;
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Best Local :
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"Crystal structure of a T-cell receptor beta-chain superantigen.";
superantigen.";
nature 384:188-192(1996).
-I- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE STAPHYLOCOCCAL FOOD POISONING SYNDROME.
-I- SIMILARITY: THE DIFFERENT S.AUREUS ENTEROTOXINS
                                                                                                                                                                                                                                                                                                                                             DISULFID SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00277; STAPH_STREP_TOXIN_1; PROSITE; PS00278; STAPH_STREP_TOXIN_2; PFAM; PF01123; Stap_Strp_toxin; 1. Enterotoxin; Toxin; Signal; Superantiques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HOVDE C.J., HACKETT S.P., BOHACH G.A.;
"Nucleotide sequence of the staphylococcal enterotoxin C3
sequence comparison of all three type C staphylococcal
enterotoxins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1991
01-NOV-1991
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P23313;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s requires a license agreement (See http://www.isb-sib.ch/announce an email to license@isb-sib.ch).
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Mismatches 36
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                                                                                                                                                                                                                                                                                     Length 266;
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Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                         dissimilarity.",

J. MOI. Biol. 269:270-280(1997).

-i- DISEASE: STAPHYLOCOCCAL ENTEROTOXING
STAPHYLOCOCCAL FOOD POISONING SYNDROW

-i- SIMILARITY: THE DIFFERENT S. AUREUS EN
                                                                                                                                                                                                                                                                                                                   MEDLINE; 97334373.
SCHAD E.M., PAPAGEORGIOU A.C., SVENSSON L.A., ACHARYA K.R.; "A structural and functional comparison of staphylococcal enterotoxins A and C2 reveals remarkable similarity and
                                                                                                                                                                                                                                                                                                                                                                                                                                 enterotoxins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Crystal structure of the superantigen enterotoxin Staphylococcus aureus reveals a zinc-binding site." Structure 3:769-779(1995).
SEQUENCE
                                                                                                                                                                                                               PIR; A60114; A60114.
                                                                                                                                                                                                                                                                                                                                                                                      COMPARISON OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWAMINATHAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BOHACH G.A., SCHLIEVERT P.M.; "Conservation of the biologically active enterotoxins C1 and C2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., MEDLINE; 89277549.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENTEROTOXIN
                                                                                                                                                                                PDB; 1STE; 23-DEC-96.
PDB; 1SE2; 08-MAR-96.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BREHM R.D., TRANTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
                                                                                                                      Enterotoxin;
                                                                                                                                       PFAM; PF01123;
                                                                                                                                                                                                                                                                                                                                                                                                                     Nat. Struct.
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                                                                                                                                                   PROSITE;
                                                                                                                                                                   ROSITE;
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                                                                                                                                                                                                                               PYROGENIC EXOTOXINS ARE ALL
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                                                                                                                                  PS00277; STAPH_STREP_TOXIN_1;
PS00278; STAPH_STREP_TOXIN_2;
01123; Stap_Strp_toxin; 1.
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(Rel. 28, Last sequence update)
(Rel. 38, Last annotation update)
TYPE C-2 PRECURSOR (SEC2).
998
                                                                                                                     Toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                   Biol.
AA;
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137
36
110
145
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                                                                                                           Signal;
27
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                                                                                                                                                                                                                                             COOD POISONING SYNDROME DIFFERENT S.AUREUS ENT
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                                                                                                                      Superantigen; Zinc;
                            ZINC.
                                                                                          ENTEROTOXIN TYPE C-2
A115FD37 CRC32;
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01-AUG-1988
01-JAN-1990
15-DEC-1998
EXOTOXIN TYP
                                                        entities
or send a
                                                                           the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See
                                                                                                                                                                                                           JOHNSON L.P., L'ITALIEN J.J., SCHLIEVERT P.M.;

"Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is related to Staphylococcus aureus enterotoxin B.";

MO1. Gen. Genet. 203:354-356(1986).

-I- DISEASE: THE STREPTOCOCCAL PYROGENIC TOXINS A, B, AND C ARE THE CAUSATIVE AGENTS OF THE SYMPTOMS ASSOCIATED WITH SCARLET FEVER, HAVE BEEN ASSOCIATED WITH STREPTOCOCCAL TOXIC SHOCK-LIKE DISEASE AND MAY PLAY A ROLE IN THE EARLY EVENTS OF RHEUMATIC
     EMBL;
PIR; !
PIR; !
                             EMBL; U40453; AAC48868.1;
EMBL; X03929; CAA27568.1;
                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE; 86284313.
                                                                                                                                                                                                                                                                                                                                                                        WEEKS C.R., FERRETTI J.J.;
"Nucleotide sequence of the ty:
(erythrogenic toxin) gene from
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus pyogenes 
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                   Infect.
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                                                                                                                                                             MISCELLANEOUS: THIS TOXIN SEEMS TO SIMILARITY: THE DIFFERENT S.AUREUS PYROGENIC EXOTOXINS ARE ALL RELATES
      A26152;
S29659;
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                                                      requires a license agreement (See an email to license@isb-sib.ch).
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990 (Rel. 13, Last sequence update)
998 (Rel. 37, Last annotation update)
998 (Rel. 37, Last annotation update)
      A26152.
S29659.
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rom Streptococcus
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01-FEB-1991
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P20723;
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SIGNAL
                "The crystal structure of staphylococcal entero In2+mediated homodinerization."; EMBO J. 15:6832-6840(1996).
-i- SUBUNIT: HOMODIMER; ZINC-DEPENDENT.
-i- DISEASE: STAPHYLOCOCCAL ENTEROTOXIONS CAUSE STAPHYLOCOCCAL FOOD POISONING SYNDROME.
-i- SIMILARITY: THE DIFFERENT S.AUREUS ENTEROTO
                                                                                                                                                                                                             Staphylococcus aureus.
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                                                                                               SEQUENCE FROM N.A.,
STRAIN-ATCC 23235;
MEDLINE; 97157473.
                                                                                                                                            enterotoxin D.
                                                                                                                                                               BAYLES
                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE; 89359112.
                                                                                                                                                                                                Bacillus/Staphylococcus
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                                                                                       SUNDSTROEM M., ABRAHMSEN
                                                                                                                                                     BAYLES K.W., IANDOLO J. "Genetic and molecular
                                                                                                                                                                                                           Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P01552; 1SEB
                                                                               OHLSTEN M.;
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         EXOTOXINS
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D PRECURSOR (SED).
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STAPH_STREP_TOXIN_2;
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K -> E (IN REF. 2).

VT -> MK (IN REF. 2).

SQEVFAQODPD -> LPKGICSTRPK (
H -> Q (IN REF. 2).

S -> N (IN REF. 2).

NLQNIYFLYEGDP -> TFKIYIFFMRV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 746; DB 1;
Pred. No. 1.08e-1
                                                                                       ANTONSSON P.,
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                  S. PYOGENES
                                                                                       MOURAD W.,
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   MEDLINE; 95354648.
SCHAD E.M., ZAITSEVA I.,
SCHLIEVERT P.M., OHLENDO
                                                                                                                                                                                                                 MEDLINE; 872;
HUANG I.-Y.,
                                                                                                                                                                                                                                             SEQUENCE OF 25-257.
MEDLINE; 87222293.
                                                                                                                                                                                                                                                                                                                                                                                                          BETLEY
                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 88086892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus/Staphylococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus aureus.
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HSSP; P13163; 1SXT.
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                                                                                                                                                                                                                                                                                                                                  JETLEY M.J., MEKALANOS J.J.,
"Nucleotide sequence of the ty
"Nucleotide 170:34-41(1988).
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                                                                                             K-RAY CRYSTALLOGRAPHY
                                                                                                                                                                                        "Complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182
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                                                                                                                                                   -Y., HUGHES J.L., BERGDOLL M.S., SCHANT: e amino acid sequence of staphylococcal Chem. 262:7006-7013(1987).
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SEVA I., ZAITSEV V.N., DOHLSTEN OHLENDORF D.H., SVENSSON L.A.;
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                                                                                             (1.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus/Clostridium group; us group; Staphylococcus.
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                                                                                                                                                                                                                                                                                                                                                                    type A staphylococcal enterotoxin gene.";
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Pred. No. 2.16e-54
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Nat. Struct "1"
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[4]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBUNIT: MONOMER.
-!- DISEASE: STAPHYLCOCOCCAL ENTEROTOXINS CAUSE THE I
-STAPHYLCOCOCCAL FOOD POISONING SYNDROME.
-!- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY A
-!- SIMILARITY: THE DIFFERENT S.AUREUS ENTEROTOXINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCHAD E.M., PAPAGEORGIOU A.C., SVENSSON L.A., ACHARYA K.R "A structural and functional comparison of staphylococcal enterotoxins A and C2 reveals remarkable similarity and dissimilarity.";
J. Mol. Biol. 269:270-280(1997).
                                                                                                                                                                  METAL
                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                              PDB; 1ESF; 11-JUL-96.
PDB; 1SEA; 15-OCT-95.
PDB; 1SXT; 19-NOV-97.
                                                                                                                                                                                                                                                                                                                                     EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPARISON OF STRUCTURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The Co-crystal structure of staphylococcal enterotoxin 2n2+ at 2.7-A resolution. Implications for major histococcomplex class II binding.";
J. Biol. Chem. 271:32212-32216(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUNDSTROEM M.,
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                                                                                                                                                                              METAL
                                                                                                                                                                                                                                    Enterotoxin;
                                                                                                                                                                                                                                              PFAM; PF01123;
                                                                                                                                                                                                                                                          PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3D-STRUCTURE MODELING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABRAHMSEN L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Crystal structure of the superantigen staphylococcal enterotoxin type A.\,^n;
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                                                                                                                                                                                                                                                                                                               A28664; A28664.
A29566; A29566.
FKNKDLADKYKDKYVDVFGANYYYQCYFSKKTNDINSHETDKRKTCMYGGVTEHNGNQLD 127
                    FDSKDIVDKYKGKKVDLYGAYYGYQC-----AGG--T--PNK-TACMYGGVTLHDNNRLT 144
                                                       DLRKKSELQGTALGNLKQIYYYNEKAKTENKESHDQFLQHTILFKGFFTDHSWYNDLLVD
                                          ELHKSSKFTGL-MENMK-VLYDDNHVSAINVKSIDQFLYFDLIYSIKDTKLGNYDNVRVE
                                                                                                                                                                                                                                                                                                                                      M18970;
                                                                                                 Similarity
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                                                                                     Score 375;
Pred. No. 2.
56; Mismatc
                                                                                                                                                                                                                                   Superantigen;
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ZINC.
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CRC32;
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staphylococcal
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                                                                                                                                                                                                                                          PROSITE; PS00277; STAPH_STREP_TOXIN_1; PROSITE; PS00276; STAPH_STREP_TOXIN_2; PFAM; PF01123; Stap_Strp_toxin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ETXE_STAAU
P12993;
                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                             EMBL; M21319; AAA26
PIR; A28179; A28179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         enterotoxins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cloning and nucleotide sequence of the type E staphylococcal enterotoxin gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus aureus.
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                                                                                                                                                                                                                                 Enterotoxin; Toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWAMINATHAN S., FUREY W.F. JR., PLETCHER RESidues defining V beta specificity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3D-STRUCTURE MODELING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUCH J.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 88257005.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         STAPHYLOCOCCAL FOOD POISONING SYNDROME. SIMILARITY: THE DIFFERENT S.AUREUS ENTEROTOXINS PYROGENIC EXOTOXINS ARE ALL RELATED.
                                                                                                              DLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTGHPWYNDLLVD 94
                                                                                                                                                                                                                                                                                    1SEE;
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         EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 204
                                 FKNKDLADKYKDKYVDVFGANYYYQCYFSKKTNDINSHETDKRKTCMYGGVTEHNGNQLD
                                                           LGSKDATNKYKGKKVDLYGAYYGYQC----AGG--T--PNK-TACMYGGVTLHDNNRLT 144
                                                                                      ELHKSSKFT-GLMENMK-VLYDDNHVSAINVKSIDQFLYFDLIYSIKDTKLGNYDNVRVE 67
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257 /
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(Rel. 13, Last sequence update)
(Rel. 38, Last annotation updat
TYPE E PRECURSOR (SEE).
                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                            AAA26617.1; -.
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                                                                                                                                                                                                                               Signal; Superantigen; 3D-structure
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                                                                                                                                        Pred.
56; N
                                                                                                                                                     Score 329; DB 1;
Pred. No. 1.15e-38;
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                                                                                                                                                                                           ENTEROTOXIN TYPE 88BA67C3 CRC32;
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                                                                                                                                         Mismatches
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P13380;
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                  CHAIN
                                                                                                                              EMBL; M35514; AAA27017.1; ALT_SEQ. EMBL; M97156; AAB59091.1; -. EMBL; M97157; AAB59092.1; -. PIR; A30509; A30509.
                                                                                                                                                                                                                                                                                                                                                                                                                 Nat. Struct. Biol. 4:635-643(1997).

-i- DISEASE: THE STREPTOCOCCAL PYROGENIC TOXINS A, B, AND C ARE THE CAUSATIVE AGENTS OF THE SYMPTOMS ASSOCIATED WITH SCARLET FEVER, HAVE BEEN ASSOCIATED WITH STREPTOCOCCAL TOXIC SHOCK-LIKE DISEASE AND MAY PLAY A ROLE IN THE EARLY EVENTS OF RHEUMATIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ROUSSEL A., ANDERSON B.F., BAKER H.M., FRASER J.D., BAKER E.N.; "Crystal structure of the streptococcal superantigen SPE-C: "City but and zinc binding suggest a novel mode of interaction with but all and a zinc binding suggest a novel mode of interaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Molecular population genetic evidence of alleles of the pyrogenic exotoxin C gene (clones of Streptococcus pyogenes."; Infect. Immun. 60:3513-3517(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REVISIONS TO 21-26.
STRAIN=T18P / MGAS 1585;
MEDLINE; 92363541.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1995 (Rel. 31, Last sequence update) 15-JUL-1998 (Rel. 36, Last annotation updat EXOTOXIN TYPE C PRECURSOR (SPE C).
                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 97397352.
ROUSSEL A., ANDERSON B.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.,
STRAIN-T18P / MGAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus pyogenes.
 SEQUENCE
                                                PFAM; PF01123;
Toxin; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 88314303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                    PROSITE;
                                                                                                                    PDB;
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                                                            PS00277; STAPH_STREP_TOXIN_1;
PS00278; STAPH_STREP_TOXIN_2;
01123; Stap_Strp_toxin; 1.
   235
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                                                 3D-structure.
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1585;
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 EXOTOXIN TYPE C. 524BB55D CRC32;
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ng pathogenic
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SEGHEZZI W., MEILI C., RUFFINER R., KUENZI R., FIECHTER A.;
                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
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15-DEC-1998 (Rel. 37
CYTOCHROME P450 52A8
                                                                                                                PROSITE; PS00086; CYTOCHROME_P450; 1.

PFAM; PF00067; p450; 1.

Electron transport; Oxidoreductase; Monooxygenase; BINDING 464 HEME (BY SIMILARITY).

SEQUENCE 517 AA; 59525 MW; D851204F CRC32;
                                                                                                                                                                                                           entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Candidaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Candida tropicalis
Eukaryota; Fungi; l
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                                                                                                                                                                                      EMBL; 213012; CAA78356.1;
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248
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                                              189
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                       36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -APR-1993
                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10
                                                                                                                                                                                                                                                                                                       INDUCTION: BY VARIOUS ALKANES.
SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DIYL 233
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                      INVKSIDQFLYFDLIYSIKDTKLGNYDNVRVEFKN-KDLADKY-KDK-YVDV--FGANYY
                                                                                                                                                                             S22974;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KLYEFNNSPYETGYIKFIENENSF-WYDMMPAPGDKFDQSKYLMMYNDNKMVDSKD-VKI 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KIYD-ATSPYVSGRIEIGTKDGKHEQIDLFDSPNEG-TRSDIFAKYKDNRIINMKNFSHF
                                            FTVDSATEFLFGESVHSLKDETIGSYQDD-IDFVGRKDFAESFNKAQEYLAIRTLVQDFY 247
 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32;
                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Candida.
                                                                     Conservative
                                                                                                                                                                           S22974
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25, Created)
25, Last sequence update)
37, Last annotation update)
2A8 (EC 1.14.14.1) (CYPLIIA8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ascomycota;
                                                                               6.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Yeast).
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Pred. No. 6.04e-10;
37; Mismatches 49
                                                                   20;
                                                                               Score 112;
Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hemiascomycetes;
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                                                                     Mismatches
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                                                                               DB 1;
.24e-02;
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                                                                                        Length 517;
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                                                                   Indels
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Q12387;
Q1-NOV-1997
Q1-NOV-1997
                                                                                                                                                                                      Q04711;
01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U36382; AAA79781.1; -.
EMBL; U54799; AAB00196.1; -.
EMBL; Z74818; CAA99086.1; -.
SGD; L0002975; DEC1.
SEQUENCE 796 AA; 92808 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a copyrence of the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TZERMIA M., KATSOULOU C., ALEXANDRAKI D.;
"Sequence analysis of a 33.2 kb segment from the chromosome XV reveals eight known genes and ten not frames including homologues of ABC transporters, phosphatases and human expressed sequence tags.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEC 1
                                              Eukaryota; Fung1; Ascomycota;
Saccharomycetaceae; Saccharomy
                                                                       Saccharomyces cerevisiae (Baker's yeast). 
Eukaryota; Fungi; Ascomycota; Hemiascomyc
                                                                                                                    TY18 OR YML044W OR YM9827.08
                                                                                                                                       01-NOV-1997 (Rel. 35, C
01-NOV-1997 (Rel. 35, L
15-DEC-1999 (Rel. 39, L
TRANSPOSON TY1 PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE; 97321807.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. HERMANN G.J., SHAW J.M.; Submitted (APR-1996) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. KINGSBURY T.J., HC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                              YME4_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yeast 13:583-589(1997).
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                                                                                                                                                                                                                                                                                                                                                            187
                                                                                                                                                                                                                                                                                                                                                                                                        103
                                                                                                                                                                                                                                                                                                                                                                                                                                                     128
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                                                                                                                                                                                                                                                                                                                                                                                                      FKFPSYELSYHWF-MKALEDSNYNQ 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KFKQSPGK-FDYNKLLEEPYGLKGTTITGDTRSLEFL-HNFFVELGK-YDEALHVYERGN 102
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DV-1997 (Rel. 35, Last seq)
DV-1997 (Rel. 35, Last ann)
PROTEIN (MDM20 PROTEIN).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19;
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cetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.0%;
llarity 22.4%;
Conservative
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                                                 Saccharomyces
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Last annotation updat
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                                                                                                                                                                                      sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 105; DB 1;
Pred. No. 2.56e-01;
24; Mismatches 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL/GenBank/DDBJ
                                                                     Hemiascomycetes;
                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                         210
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                                                                       Saccharomycetales;
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                    1009 LNANKKIITTLKKQYDTKIINLGESDNEIQYDIL-GLEIKYQRGKYMKLGMENSLTE-KI 1066
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                                                                                                                                                                                                                                              Aspartyl
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-S288C / AB972;
CONNOR R., CHURCHER C., BARRELL B.G., RAJANDREAM M.A.;
SUDMILTED (FEB-1995) to the EMBL/GenBank/DDBJ databases.
-I- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY U23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence up
15-DEC-1999 (Rel. 39, Last annotation
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Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY U23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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PROSITE; PS00141; ASP_PROTEASE; 1.
                                                                                                                                                                                                                       NP_BIND
                                                                                                                                                                                                                                                                                                     Transposable element; Hypothetical protein; Hydrolase,
                                                                                                                                                                                                                                                                                                                               PROSITE; PS00141; ASP_PROTEASE; 1.
                                                                                                                                                                                                                                                                                                                                                               EMBL; Z48430; CAA88330.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSPOSON TY1 PROTEIN B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            168 LVKNKKLYEFNNSPYETGYIKFIENENSFWYDMMPAPGDKFDQSKYLMMYNDNKMVDSKD 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   228 VKIEVYLTTK 237
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                                                                                                                                                                                                                                                                        protease; ATP-binding.
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1328 AA;
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1328
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                                                                     Score 106; DB 1;
Pred. No. 1.92e-01;
23; Mismatches 25
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Pred. No. 1.92e-01;
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W; F4A24298 CRC32;
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Q04670;
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P25384;
01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence up
15-DEC-1998 (Rel. 37, Last annotation
TRANSPOSON TY1-17 PROTEIN B.
TY1B OR YCL019W OR YCL19W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEVLIN K., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A.; Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY U23.
WARMINGTON J.R., ANWAR R., NEWLON C.S., WARING R.B., DAVIES INDGE K.J., OLLVER S.G.; "A 'hot-spot' for Ty transposition on the left arm of yeast chromosome III.";
                                                                                                                      Saccharomyces cerevisiae (Baker's yeast). Eukaryota; Fungi; Ascomycota; Hemiascomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aspartyl protease; ATP-binding.
ACT_SITE 34 34 PR
NP_BIND 1204 1211 AT
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Transposable element; Hypothetical protein; Hydrolase;
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01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation updat
                                                                                                                                                                                                                                                                                                                                   1067 PKLNVPLNPK 1076
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                                                         MEDLINE; 86205247.
                                                                          SEQUENCE FROM N.A.
                                                                                                        Saccharomycetaceae;
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23; Mismatches 25
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Best Local Similarity 29.2%;
Matches 21; Conservative
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EMBL; X59720; E264443; -.
PIR; B23496; B23496.
PIR; S19345; S19345.
Transposable element; Hypothetical protein; Hydrolase; Aspartyl protease; ATP-binding.
NP_BIND 1223 1230 ATP (POTENTIAL).
SEQUENCE 1347 AA; 154069 MW; 71FC7229 CRC32;
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SEQUENCE FROM N.A.

GENT M.E., INDGE K.J., JAMES C.M.,

STATEVA L.I.,

SUBMITTED (MAR-1992) to the EMBL/GenBank/DDBJ databases.

-I- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY U23.
                                                                                                                                                                                                                                                                       1086 PKLNVPLNPKGK 1097
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MEDLINE: 86041864.

WARMINGTON J.R., WARING R.B., NEWLON C.S., INDGE K.J., OLIVER S.G.;

"Nucleotide sequence characterization of Ty 1-17, a class II

transposon from yeast.";
                                                                                                                                                                               228 VKIEVYLTTKKK 239
                                                                                                                                                                                                                                                                                                                                                     168 LVKNKKLYEFNNSPYETGYIKFIENENSFWYDMMPAPGDKFDQSKYLMMYNDNKMVDSKD 227
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Apr 20 15:13:54 2000; MasPar time 17.90 Seconds 629.702 Million cell updates/sec

Tabular output not generated.

Title:

Description: Perfect Score: Sequence: >US-09-150-947-12 (1-239) from USO9150947.pep 1763 1 ESQPDPKPDELHKSSKFTGL.....NKMYDSKDVKIEVYLTTKKK 239

Scoring table: PAM 150 Gap 11

Searched: 142080 segs, 47172406 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Statistics:

pir62 1:pir1 2:pir2 3:pir3 4:pir4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 46.393; Variance 108.813; scale 0.426

SUMMARIES

22 22 23 24 24 25 26 27 27	Result No.
1183 1186 11156 1148 746 694 690 598 412 375 373 373 373 117 117 1117 1117 1117	Score
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6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	٥.
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ALIGNMENTS

#cross-refere #contents REFERENCE #authors #journal #title	##experime REFERENCE #authors #journal #title		#authors #journal #title #cross-refere #accession	##molecule_type DNA ##residues 1-2 ##cross-references ##cross-references ##experimental_sour REFERENCE A92065	#accossion	RESULT 1 ENTRY TITLE ORGANISM DATE ACCESSIONS
#cross-references MUID:71007901 #contents annotation; chymotryptic peptides #RENCE A92063 #authors Huang, I.Y.; Bergdoll, M.S. #authors J. Biol. Chem. (1970) 245:3493-3510 #journal Jrhe primary structure of staphylococcal enterotoxin B. I. #solation, composition, and sequence of tryptic peptides from oxidized entero-toxin B.	##experlmental_source strain S-6 A92064 A92064 AP2064 AP20664 AP20664 AP20664 AP20666 AP20664 AP206666 AP206666 AP2066666 AP2066666 AP2066666 AP20666666 AP206666666 AP20666666666666666666666666666666666666	_type protein 28-55, 'NND', 59-68, 'NE', 71, 'FDLIYL', 78-117,119-127, 'N', 129, 'D',131-132, 'ENT', 136-148, 'GN',151-156, 'Y', 157-184, 'EQ',187-232,'N',234-245,'ND',248-266 ##label HUA	#authors Huang, I.Y.; Bergdoll, M.S. J. Biol. Chem. (1970) 245:3518-3525 #title The primary structure of staphylococcal enterotoxin B. III. The cyanogen bromide peptides of reduced and aminoethylated enterotoxin B. and the complete amino acid sequence. #cross-references MUID:71007902 #accession A92065	##molecule_type DNA ##residues 1-266 ##label JON ##cross-references EMBL.M11118; NID:g152999; PIDN:AAA88550.1; ##experimental_source strain S6 NCE A92065	#authors Jones, C.L.; Khan, S.A. #authors Jones, C.L.; Khan, S.A. #journal J. Bacteriol. (1986) 166:29-33 #title Nucleotide sequence of the enterotoxin B gene from #title Staphylococcus aureus. #cross-references MUID:86168029 #across-for S2736	ENSAB6 #type complete enterotoxin B precursor - Staphylococcus aureus #formal_name Staphylococcus aureus 24-Apr-1984 #sequence_revision 15-Oct-1996 #text_change 18-Jun-1999 \$2360; A92065; S27240; A01815

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RESULT
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#title
enterotoxin C-1.
#cross-references MUID:83213327
#accession A01816
                                                                                                                                                                                   #authors Bohach, G.A.; Schlievert, P.M.
#journal Mol. Gen. Genet. (1987) 209:15-20
#title Nucleotide sequence of the staphylococcal enterotoxin
and relatedness to other pyrogenic toxins.
#cross-references_MUID:88038352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #authors Schantz, E.J.; Roessler, W.G.; Wagman, J.;
Dunnery, D.A.; Bergdoll, M.S.
#journal Biochemistry (1965) 4:1011-1016
#title Purification of staphylococcal enterotoxin
#cross-references MUID:66035792
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##molecule_type protein
##residues 28-42;128-148 ##label ALA
##residues 28-42;128-148 ##label ALA

FICATION #superfamily enterotoxin B

IFICATION 0nterotoxin; extracellular protein; toxin
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                                                                                                                    ##cross-references EMBL:X05815;
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                                                                                                                                                 ##molecule_type DNA
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Similarity 99.6%;
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enterotoxin C-1 precursor - Staphylococcus
#formal_name Staphylococcus aureus
15-Nov-1984 #sequence_revision 05-Jan-1996
18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Moskaleva, E.Y.; Sveshnikov, P.G.; Pozdnyakova
Shemchukova, O.B.; Severin, E.S.
Eur. J. Biochem. (1992) 209:823-828
Identification of functionally active fragments
staphylococcal enterotoxin B.
                                               AO1816
Schmidt, J.J.; Spero, L.
J. Blol. Chem. (1983) 258:6300-6306
The complete amino acid sequence of
                                                                                                                                                                       S06356
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                                                                                                    1-266 ##label BOH
1-266 ##label BOH
--- EMBL:X05815; NID:946566; PIDN:CAA29260.1;
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#disulfide_bonds #status experimental

yth 266  #molecular-weight 31436  #checksum 4249
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Pred. No. 2.96e-284;
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                                               Staphylococcal
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kova, L.P.;
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Best Local :
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                                                                                                                                                                                                                   ##residues 1-266 ##label HOV
##cross-references GB:x51661; NID:g46570; PIDN:CAA35972.1; PID:g46571
#FICATION #superfamily enterotoxin B
#length 266 #molecular-weight 30671 #checksum 6135
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                                                                                                              28 ESQPDPMPDDLHKSSEFTGTMGNMKYLYDDHYVSATKVKSVDKFLAHDLIYNISDKKLKN
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                                               YDKYKTELLNEDLAKKYKDEVVDVYGSNYYVNCYFSSK-DNV-GKVTGG-KTCMYGGITK 144
                                                                                           ESQPDPKPDELHKSSKFTGLMENMKVLYDDNHVSAINVKSIDQFLYFDLIYSIKDTKLGN 60
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HEGNHFDNGNLQNVLVRVYENKRNTISFEVQTDKKSVTAQELDIKARNFLINKKNLYEFN
                             YDNVRVEFKNKDLADKYKDKYVDVFGANYYYQCYFSKKTNDINSHETDKRKTCMYGGVTE 120
                                                                                                                                                            159;
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l Similarity 66.8%;
l61; Conservative
                                                                                                                                                                         h 65.6%;
Similarity 66.0%;
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enterotoxin C3 - Staphylococcus aureus
#formal_name Staphylococcus aureus
19-Mar-1997 #sequence_revision 19-Mar-1997
16-Jul-1999
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#length 266 #molecular-weight 30546 #che
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#product enterotoxin C-1 #status experimental #label
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Pred. No. 1.19e-1
40; Mismatches
                                                                                                                                                                         Score 1156; DB 2;
Pred. No. 7.73e-176;
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Best Local Similarity 65.6%;
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#journal J. Bacteriol. (1989) 171:4507-4510
#title Nucleotide sequence of the type C-3 staphylococcal
enterotoxin gene suggests that intergenic recomb
Causes antigenic variation.
#cross-references_MJID:89327174
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#title Conservation of the biologically active
#taphylococcal enterotoxins C1 and C2.
#cross-references MUID:89277549
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179
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##residues 28-66 ##label BOH2
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                                    205
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##cross-references GB:M28364; NID:g153003; PIDN:AAA26624.1; PID:g153004
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NSPYETGYIKFIENE-NSFWYDMMPAPGDKFDQSKYLMMYNDNKMVDSKDVKIEVYLTTK
                                                                                      HEGNHEDNGNLQNVLIRVYENKRNTISFEVQTDKKSVTAQELDIKARNFLINKKNLYEEN 204
                                                                                                                                            YDNVRVEFKNKDLADKYKDKYVDVFGANYYYQCYFSKKTNDINSHETDKRKTCMYGGVTE 120
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                                                                     HNGNQLDK-Y-RSITVRVFEDGKNLLSFDVQTNKKKVTAQELDYLTRHYLVKNKKLYEFN 178
                                                                                                                                                                               YDKVKTELLNEDLAKKYKDEVVDVYGSNYYVNCYFSSK-DNV-GKVTGG-KTCMYGGITK 144
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Bohach, G.A.; Schlievert, P.M.
57:2249-2252
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enterotoxin C-2 precursor - Staphylococcus aureus
enterotoxin C-3 precursor
#formal_name Staphylococcus aureus
10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change
16-Jul-1999
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                                                                                                                                                                                                                                                                                             Conservative
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#product enterotoxin C-2 #status predicted #labe
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                                                                                                                                                                                                                                                                                             40;
                                                                                                                                                                                                                                                                                                              Score 1148; DB 2; Pred. No. 2.05e-174;
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                                                                                                                                                                                                                                                                                                                              Length 266;
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#journal
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#cross-references MUID:86166804
#accession S29659
                                    #accession
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##molecules_type DNA
##cross-references GB:U40453; EMBL:M19350; NID:g1877426;
##cross-references GB:U40453; EMBL:M19350; NID:g1877430
                                                                                                                                                                                                                                                                                                                                                                                                                       238
                                                                                      ##experimental_source Streptococcus pyogenes strain
Arizona unassigned phage
                                                                                                                                                                                                                                     ##note
                                                                                                                                                                                                                                                      ##experimental_source Streptococcus pyogenes strain
Texas unassigned phage
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##experimental_source Streptococcus pyogenes strain MGAS156 isolate
Nebraska unassigned phage
##molecule_type DNA
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Characterization and clonal distribution of four alleles of the spea gene encoding pyrogenic exotoxin A (scarlet fever
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  erythrogenic toxin; scarlet fever toxin
#formal_name Streptococcus pyogenes phage T12
10-Sep-1999 #sequence_revision 10-Sep-1999 #t
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                                    S18796
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:9659; S18782; S18784; S18785; S18791; S18796;
                                                                      the nucleotide sequence was submitted
                                                                                                                                           9-244 ##label NEY
                                                                                                                                                                              nucleic acid sequence not shown;
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Best Local :
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31-251
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#cross-references
#accession S187
##status
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Zealand unassigned phage
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##experimental_source Streptococcus pyogenes strain MGAS494 isolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 NGNQLDKYRSITVRVFEDGKNLLSFDVQTNKKKVTAQELDYLTRHYLVKNKKLYEFNNSP 181
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Similarity 50.2%;
119; Conservative
                                                    Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
J. Exp. Med. (1991) 174:1271-1274
Characterization and clonal distribution of four alleles of the spea gene encoding pyrogenic exotoxin A (scarlet fever toxin) in Streptococcus pyrogenes.
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S18782
                                                                                                                                                                                                                                                                                                scarlet fever toxin
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exotoxin A precursor (allele 4) - Streptococcus pyogenes
(strain MGAS262 isolate California) (fragment)
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#product exotoxin type A #status predicted #label 
#length 251 #molecular-weight 29246 #checksum 1475
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#superfamily enterotoxin
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strain MGAS262 isolate California
29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change
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nucleic acid
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Pred. No. 1.75e-103;
43; Mismatches 59;
sequence
not shown;
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#authors
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                                                                                                                                                                                                                                                                                                                                                                                                                                       #journal #title
                                                                                                                                                                                                                                                                                                                                           #title Characterization and clonal distribution of four alleles of the speA gene encoding pyrogenic exotoxin A (scarlet fever toxin) in Streptococcus pyogenes.

#cross-references MUID:92044323
#accession $18783
                                                                                                                                                             #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #variety
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-236
##residues 1-236 ##label NEA ##cross-references EMBL:X61569; NID:g47313; PIDN:CAA43767.1; PID:g47314 ##experimental_source strain MGAS485 isolate Yugoslavia unassigned phagus ##experimental_source strain MGAS485 isolate Yugoslavia unassigned phagus ##note the nucleotide sequence was submitted to the EMBL Data ##note
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##cross-references EMBL:X61573; NID:g47303;
##note the nucleotide sequence was
Library, September 1991
                                                                                                                                                                              ##cross-references EMBL:X61568; NID:947289; PIDN:CAA43766.1; PID:947290 ##experimental_source strain MGAS158 isolate Nebraska unassigned phage the nucleotide sequence was submitted to the EMBL Data Library, September 1991
                                                                                                              ##molecule_type DNA
                                                                                                                                                                                                                                                                                               ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                         ##status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 DNVRVEFKNKDLADKYKDKYVDVFGANYYYQCYFSKKTNDINSHETDKRKTCMYGGVTEH 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 SQPDPKPDELHKSSKFTGLMENMKVLYDDNHVSAINVKSIDQFLYFDLIYSIKDTKLGNY 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGNHLEIPKNILVKVSIDGIQSLSFDIETSKKMVTAQELDYKVRKHLTDNKQLYTNGPSK 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NGNQLDKYRSITVRVFEDGKNLLSFDVQTNKKKVTAQELDYLTRHYLVKNKKLYEFNNSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39.98;
1 Similarity 46.58;
107; Conservetion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #formal_name Streptococcus pyogenes phage
strain MGAS188 isolate webraska; strain MGAS485 isolate
Yugoslavia; strain MGAS491 isolate United Kingdom; strain
MGAS624 isolate Germany; strain MGAS495 isolate Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M. J. Exp. Med. (1991) 174:1271-1274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             $18783 #type fragment exotoxin type A precursor (allele 3) - Streptococcus phage (strain MGAS158 isolate Nebraska and others)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         speA
#superfamily enterotoxin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S18783; S18793; S18794; S18801; S18798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change
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                                                                                                                                   nucleic acid sequence not shown; translation
                                                                                                                                                                                                                                                                                                                         nucleic acid sequence not shown;
                                                                                       1-236 ##label NEA
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Pred. No. 3.53e-96;
53; Mismatches 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (fragment) #status
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EMBL Data
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                                                                                                                                                                                                                                                                                                                                                                                            189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##experimental_source strain MGAS495 isolate Germany unassigned phage the nucleotide sequence was submitted to the EMBL Data Library, September 1991
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##experimental_source strain MGAS624 isolate Germany unassigned phage
the nucleotide sequence was submitted to the EMBL Data
Library, September 1991
                                                                                                                                                                                                                                                                                                                                                     182
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Local Similarity 48.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DKLKTELKNQEMATLFKDKNIDIYGVEYYHLCYLC----E-NA-E---RSACIYGGVTNH 128
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                                                                                                                                                                                                                                                                                                                                                   YETGYIKFI-ENENSFWYDMMPAPGDKFDQSKYLMMYNDNKMVDSKDVKI 230
                                                                                                                                                                                                                                                                                                                                                                                        YETGYIKFIPKNKESFWFDFFPEP-E-FTQSKYLMIYKDNETLDSNTSQI 236
                                                                                                                                                                                                                                                                                                                                                                                                                              NGNQLDKYRSITVRVFEDGKNLLSFDVQTNKKKVTAQELDYLTRHYLVKNKKLYEFNNSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSK 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNVRVEFKNKDLADKYKDKYVDVFGANYYYQCYFSKKTNDINSHETDKRKTCMYGGVTEH 121
S18786;
S18782
                                                                                                                                                                                                        s18786 #type fragment
exotoxin type A precursor (allele 2) - Stre
phage (strain MGAS250 isolate California
(fragment)
                                                                                                             #formal_name Streptococcus pyogenes phage
strain MGAS250 isolate California; strain MGAS251 isolate
California; strain MGAS256 isolate California; strain
MGAS285 isolate Colorado; strain MGAS480 isolate
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#superfamily enterotoxin
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                                                    29-Jan-1993 #sequence_revision
                                                                                                                                                                                              scarlet fever toxin
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                                                                        MGAS496 isolate Germany
                                      16-Jul-1999
                                                                                             Yugoslavia; strain MGAS492 isolate United Kingdom; strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the nucleotide sequence was submitted to the EMBL Data Library, September 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #product exotoxin type A (fragment)
#label MAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1-236 ##label NEO
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                    S18787; S18788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #checksum 612
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Pred. No. 1.92e-94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44; Mismatches
                    S18790;
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                                                      29-Jan-1993 #text_change
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                    S18792;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 16;
                                                                                                                                                                                                                                                    Streptococcus
                    S18795; S18799
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CLASSIFICATION KEYWORDS
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##note the nucleotide sequence was submitted to the EMBL Data
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##experimental_source strain MGAS285 isolate Colorado unassigned phage
##note the nucleotide sequence was submitted to the EMBL Data
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##experimental_source strain MGAS256 isolate California unassigned phag-
##note the nucleotide sequence was submitted to the EMBL Data
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##experimental_source strain MGAS480 isolate Yugoslavia unassigned phage
##acxperimental_source strain MGAS480 isolate Yugoslavia unassigned phage
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Characterization and clonal distribution of four alleles of the spea gene encoding pyrogenic exotoxin A (scarlet fever
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DKLKTELKNQEMATLFKDKNVDIYSVEYYHLCYLC---E-NA-E---RSACIYGGVTNH 128
                                                                                                                                                           YIKFI-ENENSFWYDMMPAPGDKFDQSKYLMMYNDNKMVDSKDVKIEVYLTTK 237
                                                                                                                                                                                                                          LDKYRSITVRVFEDGKNLLSFDVQTNKKKVTAQELDYLTRHYLVKNKKLYEFNNSPYETG
                                                                                                                                                                                                                                                                                                                                                      PKPDELHKSSKFTGLMENMKVLYDDNHVSAINVKSIDQFLYFDLIYSIKDTKLGNYDNVR 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SQPDPKPDELHKSSKFTGLMENMKVLYDDNHVSAINVKSIDQFLYFDLIYSIKDTKLGNY 61
                                                                                                                                                                                                                                                                                                                                                                                                                    h 33.9%;
Similarity 43.8%;
102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A26152
A26152
             26-Aug-1999
A33953
                                         A33953 #type complete
enterotoxin D precursor - Staphylococcus aureus
#formal_name Staphylococcus aureus
09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   exotoxin #molecular-weight 29168 #checksum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #superfamily enterotoxin B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          scarlet fever toxin; SPE type A (speA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A26152 #type complete streptococcal pyrogenic exotoxin Streptococcus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39.1%;
larity 48.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #formal_name Streptococcus sp.
10-Sep-1999 #sequence_revision 10-Sep-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1-250 ##label JOH
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 598; DB 1; Le
Pred. No. 7.07e-78;
47; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 690; DB 2;
Pred. No. 9.49e-94;
44; Mismatches 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 250;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #cross-references MUID:88086892
#accession A28664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #title Genetic and molecular analyses staphylococcal enterotoxin D. #cross-references MUID:89359112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #journal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##cross-references GB:m18970; NID:g153120; PID:g153121
##cross-references GB:m18970; NID:g153120; PID:g153121
##experimental_source strain FRI37
[FICATION #superfamily enterotoxin B
ty #length 257 #molecular-weight 2007
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##croos-references GB.w28521; NID:g1492109; PID:g758691
##CICATION #superfamily enterotoxin B
FICATION #superfamily enterotoxin B
William William
                                                                                                                               145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143
   205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125
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Local Similarity 36.6%;
hes 87; Conservative
                                                                                                                                                                                               83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 RVEFKNKDLADKYKDKYVDVFGANYYYQCYFSKKTNDINSHETDKRKTCMYGGVTEHNGN 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 KPDELHKSSKFTGL-MENMKYLYDD-NHVSAINVKSIDQFLYFDLIYSIKDTKLGNYDNV 64
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                                                                                                                                                                                                                                                                                                                                                                                        DLRKKSELQGTALGNLKQIYYYNEKAKTENKESHDQFLQHTILFKGFFTDHSWYNDLLVD
                                                                                                                                                                                                                             FDSKDIVDKYKGKKVDLYGAYYGYQC----AGG--T--PNK-TACMYGGVTLHDNNRLT 144
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                                                                                                                                                                                                                                                                                                                           ELHKSSKFTGL-MENMK-VLYDDNHVSAINVKSIDQFLYFDLIYSIKDTKLGNYDNVRVE 67
RGLIVFHTSTEPSVNYDLFGAQGQ-YSNT-LLRIYRDNKTINSENMHIDIYLYT 256
                                                                                                                            EEKKVPINLWLDGKQNTVPLETVKTNKKNVTVQELDLQARRYLQEKYNLYNSDVFDGKVQ
                                                                                                                                                                                            FKNKDLADKYKDKYVDVFGANYYYQCYFSKKTNDINSHETDKRKTCMYGGVTEHNGNQLD 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                 21.3%;
Similarity 35.0%;
82; Conservation
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J. Bacteriol. (1989) 171:4799-4806
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #formal_name Staphylococcus aureus 30-Jun-1989 #sequence_revision 30-
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Pred. No. 2.:
56; Mismatcl
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Pred. No. 1.85e-46.
53; Mismatches 7!
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2.27e-40;
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Best Local :
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Best Local
                                                                                                                                                                                                                                                            #authors Couch, J.L.; Soltis, M.T.; Betley, M.J.
#journal J. Bacteriol. (1988) 170:2954-2960
#title Cloning and nucleotide sequence of the
enterotoxin gene.
#cross-references_MUID:88257005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #map_position
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #authors Huang, I.Y.; Hughes, J.L.; Bergdoll, M.S.; Schantz, E.J.
#journal J. Biol. Chem. (1987) 262:7006-7013
#title Complete amino acid sequence of staphylococcal enterotoxin
#cross-references_MUID:87222293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ‡gene
                                                                                                                                                 ##residues 1-257 ##label COU
##cross-references GB.M21319; NID:g153001; PID:g153002
##CTOXION #superfamily enterotoxin B
#IEOATION #superfamily enterotoxin B
#Length 257 #molecular-weight 29358 #checl
                                                                                                                                                                                                                     ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 TGYIKF-IENENSFWYDMMPAPGDKFDQSKYLMMYNDNKMVDSKDVKIEVYLTT 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##molecule_type protein
##residues 1-233 ##label HUA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
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 10
                                     35 DLRKKSELQRNALSNLRQIYYYNEKAITENKESDDQFLENTLLFKGFFTGHPWYNDLLVD 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 DLRKKSELQGTALGNLKQIYYYNEKAKTENKESHDQFLQHTILFKGFFTDHSWYNDLLVD 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 21.2%;
Local Similarity 35.0%;
nes 82; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KYRSITVRVFEDGK-NLLSFD-VQTNKKKVTAQELDYLTRHYLVKNKKLYEFN--NSPYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EEKKVPINLMLDGKQNTVPLETVKTNKKNVTVQELDLQARRYLQEKYNLYNSDVFDGKVQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FKNKDLADKYKDKYVDVFGANYYYQCYFSKKTNDINSHETDKRKTCMYGGVTEHNGNQLD 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FDSKDIVDKYKGKKVDLYGAYYGYQC----AGG--T--PNK-TACMYGGVTLHDNNRLT 120
ELHKSSKFT-GLMENMK-VLYDDNHVSAINVKSIDQFLYFDLIYSIKDTKLGNYDNVRVE 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELHKSSKFTGL-MENMK-VLYDDNHVSAINVKSIDQFLYFDLIYSIKDTKLGNYDNVRVE 67
                                                                            Similarity 79; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entA
1 6
#length 233
                                                                                                                                                                                                                                                                                                                                                                                                          enterotoxin E precursor - Staphylococcus aureus #formal_name Staphylococcus aureus 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change
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05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change
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                                                                                          18.7%;
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A - Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #type complete
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Pred. No. 4.82e-40;
56; Mismatches 77;
                                                                        Score 329; DB 2; L
Pred. No. 6.51e-33;
56; Mismatches 80;
                                                                                                           Length 257
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RESULT
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Best Local
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#title
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#accession A30509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##residues 1-235 ##label GOS ##cross-references GB:M35514; NID:g153820; PID:g153821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        230 DIYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 MYGGVTEHNGNQLDKYRSI-TVRVFEDGKNLLSFDVQTNKKKVTAQELDYLTRHYLVKNK 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113 IYGGITPAQNNKVN-HKLLGNLFISGESQQNLNNKIILEKDIVTFQEIDFKIRKYLMDNY 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##molecule_type
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KIYD-ATSPYVSGRIEIGTKDGKHEQIDLFDSPNEG-TRSDIFAKYKDNRIINMKNFSHF 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KYRSITVRVFEDGKNL-LSFD-VQTNKKKVTAQELDYLTRHYLVKNKKLYEFNN-SP-YE
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Similarity 25.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        233
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Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.;
Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessieres, P.;
Bolotin, A.; Borchert, S.; Boriss, R.; Boursier, L.; Brans,
A.; Braun, M.; Brignell, S.C.; Bron, S.; Brouillet, S.;
Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
Choi, S.K.; Codani, J.J.; Connerton, I.F.; Cummings, N.J.;
Daniel, R.A.; Denizot, F.; Devine, K.M.; Duesterhoeft, A.;
Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.;
Fabret, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Fujita,
M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galleron, N.; Ghim,
S.Y.; Glaser, P.; Goffeau, A.; Golightly, E.J.; Grandi, G.;
Guiseppi, G.; Guy, B.J.; Haga, K.; Halech, J.; Harwood,
C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.;
Hullo, M.F.; Itaya, M.; Jones, L.; Joris, B.; Karamata, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 exotoxin
#length 235 #molecular-weight 27560 #checksum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Goshorn, S.C.; Schlievert, P.M.
Infect. Immun. (1988) 56:2518-2520
Nucleotide sequence of streptococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A30509 #type complete
exotoxin C precursor - Stre
#formal_name Streptococcus
31-Dec-1988 #sequence_revis
                                                                                                                                                                                                                                                                                                                        D69832
                                                                                                                                                                                                                                                                                                                                                           #formal_name Bacillus subtilis
05-Dec-1997 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                       D69832 #type complete
probable Rieske [2Fe-2S] iron-sulfur protein
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Pred. No. 4.19e-08;
37; Mismatches 49; Indels
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#gene
CLASSIFICATION
                                                                                                                                                                                                                                                           Query Match 6.6%;
Best Local Similarity 28.9%;
Matches 24; Conservative
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463,465,481,484
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#title
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                                                                                                                          172 KKLYEFNNSPYETGYIKFIENEN 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##molecule_type DNA
1-509 ##label KUN
##cross-references GB:Z99109; GB:AL009126; NID:g2633260; PID:e1183041;
PID:g2633375
##experimental_source strain 168
                                                         98 ARLY-YEANQNAIDYIKGIVDEH 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Y: Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.;
Kurita, K.; Lapidus, A.; Lardinois, S.; Lauber, J.;
Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.;
Maueel, C.; Medigue, C.; Medina, N.; Mellado, R.P.; Mizuno,
M.; Moestl, D.; Nakai, S.; Noback, M.; Noone, D.; O'Reilly,
M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro,
V.; Pohl, T.M.; Portetelle, D.; Porwolik, S.; Prescott,
A.M.; Presecan, E.; Pujic, P.; Purnelle, B.; Rapoport, G.;
Rey, M.; Reynolds, S.; Rieger, M.; Rivolta, C.; Rocha, E.;
Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon, E.;
Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.;
Sekowska, A.; Seror, S.J.; Serror, P.; Shin, B.S.; Soldo,
B.; Sorokin, A.; Tacconi, E.; Takagi, T.; Takahashi, H.;
Takemaru, K.; Takeuchi, M.; Tanakasi, T.;
Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, S.;
Vandenbol, M.; Vannier, F.; Vassarotti, A.; Viari, A.;
Wambutt, R.; Wedler, E.; Wedler, H.; Weitzenegger, T.;
Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto,
K.; Yata, K.; Yoshida, K.; Yoshikawa, H.F.; Zumstein, E.;
Yoshikawa, H.; Danchin, A.
Nature (1997) 390:249-256
The complete genome sequence of the Gram-positive bacterium
Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                     #length 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #superfamily Rieske [2Fe-2S] homology
2Fe-2S; metalloprotein; Rieske iron-sulfur protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D69832
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                                                                                                                                                                                                                                                                                                                                                                                     #domain Rieske [2Fe-2S] homology #label RSK\
#binding_site 2Fe-2S cluster (Cys, His, Cys, His)
(covalent) #status predicted
gth 509 #molecular-weight 57109 #checksum 4843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             preliminary; nucleic acid sequence not shown;
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                                                                                                                                                                                                                                                           Score 117; DB 2; Le
Pred. No. 5.91e-02;
24; Mismatches 28;
                                                                                                                                                                                                                                                                                                                        Length 509;
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Search completed: Thu Apr 20 15:16:21 2000 Job time : 147 secs.

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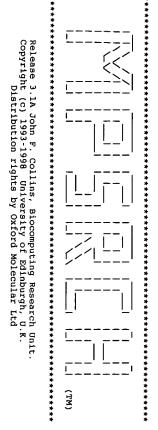
FEATURE

KEYWORDS

SUMMARY

GENETICS

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm Run on:

Thu Apr 20 15:09:54 2000; MasPar time 26.18 Seconds 632.994 Million cell updates/sec

Title: >US-09-150-947-12
Description: (1-239) from US09150947.pep
Perfect Score: 1763
Sequence: 1 ESQPDPKPDELHKSSKFTGL.....NKMVDSKDVKIEVYLTTKKK 239

Tabular output not generated.

Searched: 225878 seqs, 69334122 residues

Scoring table:

PAM 150 Gap 11

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: sptrembl12
1:sp_archea 2:sp_

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mamma1 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 45.381; Variance 98.387; scale 0.461

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

18 19 20	15 16	11 12 14	10	765	4 3 2 1	Result No.
308 244 205	694 395	718 710 704 696	1085 1084 1081	1150 1145 1143	1191 1169 1162 1153	Score
17.5 13.8 11.6		39 39 39	61	64.9 64.8	67.6 65.9	Query Match
241 179 234	236 236 268	258 258 236	260 260	239 239 239	239 239 239	Length
N N N	222	2222	222	0001	2222	DB
Q53585 Q52075 Q9X5C7	Q54779 Q57453 Q85217	085382 Q9ZNF2 Q54696 P97163	Q54739 Q54971 Q54738	Q06533 Q06535 Q065157	Q53678 Q53634 Q06532 Q06532	ID
ENTEROTOXIN H PRECURSO ENTEROTOXIN D. EXOTOXIN G PRECURSOR.	A EXOTOXIN A EXOTOXIN ROTOXIN J.	EXTRACELLULAR ENTEROTO ENTEROTOXIN TYPE GY. TYPE A EXOTOXIN PRECUR TYPE A EXOTOXIN PRECUR	SUPERANTIGEN SSA. SUPERANTIGEN. SUPERANTIGEN SSA.	H :	ENTEROTOXIN (FRAGMENT) ENTEROTOXIN TYPE C (SE ENTEROTOXIN TYPE C-7 (ENTEROTOXIN TYPE C-4 (Description
1.41e-21 2.97e-15	9.98e-103 5.63e-102 1.09e-47	3.06e-107 9.79e-106 1.32e-104 4.20e-103	3.41e-177 5.31e-177 2.01e-176	291	1.27e-197 2.24e-193 5.02e-192 2.73e-190	Pred. No.

45	44	43	42	41	40	39	38	37	36	35	34	ω	32	31	30	29	28	27	26	25	24	23	22	21
106	106	106	106	106	108	108	108	109	110	110	110	109	113	112	114	117	117	119	119	130	144	148	148	150
6.0	6.0	6.0	6.0	6.0	6.1	6.1	6.1	6.2	6.2	6.2	6.2	6.2	6.4	6.4	6.5	6.6	6.6	6.7	6.7	7.4	8.2	8.4	8.4	8.5
1793	1755	1755	1755	1755	1423	226	225	1029			198	127	1749	208	689	592	509	532	532	256	242	236	206	242
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013535	Q03612	Q12414	Q12088	Q12269	097230	Q59058	067405	Q9Y8G5	080378	066775	Q9YW62	095329	Q99337	Q25804	067296	051094	007622	061727	061726	Q9X9R8	085383	Q9x5C8	Q54512	054476
YHR214C-BP.	TRANSPOSON TY PUTATIVE		CHROMOSOME XII READING	CHROMOSOME VII READING	PFC0195W PROTEIN.	HYPOTHETICAL PROTEIN M	HYPOTHETICAL 26.1 KD P	NAD-SPECIFIC GLUTAMATE	181 (FRAGMENT).	HYPOTHETICAL 47.1 KD P	ORF MSV030 HYPOTHETICA	HYPOTHETICAL 14.5 KD P	CHROMOSOME XIV READING	COMPLETE GENE MAP OF P	FERROUS IRON TRANSPORT	PEPTIDASE, PUTATIVE.	HYPOTHETICAL 57.1 KD P	CARBOXYLESTERASE.	CARBOXYLESTERASE.	SPEX-2 PROTEIN PRECURS	EXTRACELLULAR ENTEROTO	EXOTOXIN H PRECURSOR.	T1M1 ISOLATE SWE88 SPE	ENTEROTOXIN.
5.15e-01	5.15e-01	5.15e-01	5.15e-01	5.15e-01	2.93e-01	2.93e-01	2.93e-01	2.21e-01	1.66e-01	1.66e-01	1.66e-01	2.21e-01	7.02e-02	9.37e-02	5.25e-02	2.18e-02	2.18e-02	1.20e-02	1.20e-02	4.20e-04	4.83e-06	1.30e-06	1.30e-06	6.74e-07

ALIGNMENTS

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PROSITE; PS00278; STAPH_STREP_TOXIN_1; 1. PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1. PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1. Enterotoxin. 1	PRELIMINARY; PRT; 23 (TIEMBLrel 01, Created) (TIEMBLrel 01, Last sequen (TIEMBLrel 12, Last annota (FRAGMENT). Cus aureus. irmicutes; Bacillus/Clostrid aphylococcus group; Staphylo aphylococcus group; Staphylo 0M N.A. 011313. LYON J.D., ROBERSON J.R., LU ZALION of novel type C staph and evolutionary implication of evolutionary implication of; AAA26620.1; 1; 1SE2.

179

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01-NOV-1996
01-NOV-1996
01-NOV-1999
                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TREMBLrel. 01, Last sequence update)
01-NOV-1999 (TREMBLrel. 12, Last annotation update)
ENTEROTOXIN TYPE C-7 (SEC740N) (FRAGMENT).
Staphylococcus aureus.
Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MARR J.C., LYON J.D., ROBERSON J.R., LUPHER M., BOHACH G.A.; "Characterization of novel type C staphylococcal enterotoxins: biological and evolutionary implications."; Infect. Immun. 61:4254-4262(1993).

11- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATIONS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFAM; PF01123; Stap_Strp_toxin; 1. Enterotoxin; Toxin; Superantigen.
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                                    SEQUENCE FROM
                                                                                    Bacillus/Staphylococcus
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SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
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                                                                                                                                                                                                                                                                                               PRELIMINARY;
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Q06531;
                                                                                                                                                                                                  EMBL;
HSSP;
                                                                                                                                                                                                                                                                       MEDLINE; 94011313.

MARR J.C., LYON J.D., ROBERSON J.R., LUPHER M., BOHAC "Characterization of novel type C staphylococcal ente biological and evolutionary implications.";
Infect. Immun. 61:4254-4262(1993).
I-- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE IN STAPHYLOCOCCAL FOOD POISONING SYNDROME.

-!- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence up
01-NOV-1999 (TrEMBLrel. 12, Last annotation
ENTEROTOXIN TYPE C-4 (SEC4446) (FRAGMENT).
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SEQUENCE
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"Characterization of novel type C staphylococcal enterotoxins:
biological and evolutionary implications.";
Infect. Immun. 61:4254-4262(1993).
-I- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus aureus.
Bacteria; Firmicutes; Bacillus/Clostridium
                                                                                                    SEQUENCE
                                                                                                                                                   Enterotoxin; Toxin;
                                                                                                                                                                          PFAM; PF01123; Stap_Strp_toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-4446;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 94011313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238 N
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                                                                                                                                                                                                                                                   PYROGENIC EXOTOXINS ARE ALL RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSPYETGYIKFIENNGNTFWYDMMPAPGDKFDQSKYLMMYNDNKTVDSKSVKIEVHLTTK 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HEGNHEDNGNLQNVLVRVYENKRNTISFEVQTDKKSVTAQELDIKARNELINKKNLYEEN 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YDKVKTELLNEDLAKKYKDEVVDVYGSNYYVNCYFSSK-DNV-GKVTGG-KTCMYGGITK 117
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                                                                                                                                                                                                    L13374; AAA26618.1; P34071; 1SE2.
  l Similarity
158; Conser
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159; Conser
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65.4%;
larity 65.6%;
Conservative
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Score 1153; DB 2;
Pred. No. 2.73e-190;
41; Mismatches 36;
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Pred. No. 5.02e-192;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus
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                                                                                                    52B18853 CRC32;
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                                              Length 239;
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                                                                                                                                                                                                                                                                               S. PYOGENES
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Best Local S
Matches 15
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Q06533;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1996 (TrEMBLrel. 10, Last sequence update)
Q1-NOV-1999 (TrEMBLrel. 12, Last annotation update
ENTERCTOXIN TYPE C (SECCOPELAND) (FRAGMENT).
Staphylococcus aureus.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-MNCOPELAND;
MEDLINE; 94011313.
MARR J.C., LYON J.D., ROBERSON J.R., LUPHER M., BOHACH G.A.;
"Characterization of novel type C staphylococcal enterotoxins:
"Characterization of novel type C staphylococcal enterotoxins:
blological and evolutionary implications.";
Infect. Immun. 61:4254-4262(193).
-1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
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SIMILARITY: THE DIFFERENT S. AUREUS ENT
PYROGENIC EXOTOXINS ARE ALL RELATED.
L; L13378; AAA26622.1;
P; P344771; 1STE.
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                                                  HEGNHFDNGNLQNVLIRVYENKRNTISFEVQTDKKSVTAQELDIKARNFLINKKNLYEFN
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                                                                                 SSPYETGYIKFIENNGNTFWYDMMPAPGDKFDQSKYLMMYNDNKTVDSKRVKIEVHLTTK
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Pred. No. 1.03e-189;
39; Mismatches 37;
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EDWARDS V.M., DERINGER J.R., CALLANTINE S.D., DEOBALD C.
BERGER P.H., KAPUR V., STAUFFACHER C.V., BOHACH G.A.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                Staphylococcus intermedius.

Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
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01-JUL-1997 (TrEMBLrel. 12, Las
01-NOV-1999 (TrEMBLrel. 12, Las
TYPE C ENTEROTOXIN (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enterotoxin; Toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P23313; PFAM; PF01123;
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llarity 64.3%;
Conservative
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04, Last sequence update)
12, Last annotation update)
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Pred. No. 9.52e-189;
44; Mismatches 36;
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(FRAGMENT).
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                                                                      C.F
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RESULT RESULT OF THE PROPERTY 
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Matches 15
                                                                                         Query Match
Best Local :
                                                                    Matches
                                                                                                                                                  Streptococcus pyogenes.";
Infect. Immun. 64:1161-1165(1996).
EMBL; U48794; AAB02150.; -.
EMBL; U48792; AAB02148.1; -.
HSSP; P01552; ISE3.
PFAM; PF01123; Stap_Strp_toxin; 1.
PRINTS; PR00279; BACTRLTOXIN.
SEQUENCE 260 AA; 29767 MW; C8144
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Q54739; Q54737;
Q1-NOV-1996 (TIEMBLIEL 01
01-NOV-1996 (TIEMBLIEL 01
01-NOV-1999 (TIEMBLIEL 11;
SUPERANTIGEN SSA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE; 94222556.
REDA K.B., KAPUR V., PRICH R.R.;
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HSSP; P23313; 1JCK.
PROSITE; PS00277; STAPH_STREP_TOXIN_1;
PROSITE; PS00278; STAPH_STREP_TOXIN_2;
PFAM; PF01123; Stap_Strp_toxin; 1.
NON_TER 1 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Molecular characterization and phylogenetic distribution of the streptococcal superantigen gene (ssa) from Streptococcus pyogenes Infect. Immun. 62:1867-1874(1994).
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE; 96178602.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus pyogenes. Bacteria; Firmicutes; F
                                                                                                                                                                                                                                                                                                                                          "Phylogenetic distribution
variants provides evidence
                                                                                                                                                                                                                                                                                                                                                                                  REDA K.B., KAPUR V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus.
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                                                                  l Similarity
149; Conser
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157; Conser
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                                                                  61.5%;
llarity 62.6%;
Conservative
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                                                                                                                                                                                                                                                                                                                                     GOELA D., LAMPHEAR J.G., MUSSER J.M., R bution of streptococcal superantigen SSA idence for horizontal transfer of ssa wit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLLICK J.A.,
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Pred. No. 2.31e-188;
41; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
                                                                  Score 1085; DB 2;
Pred. No. 3.41e-177;
38; Mismatches 44;
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                                                                                                                                                           C81448C1 CRC32;
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EMBL; L29565; AAA65928.1; -
HSSP; P01552; LSE3.
PFAM; PF01123; Stap_Strp_toxin; 1.
PRINTS; PR00279; BACTRLTOXIN.
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Bacteria; Firmicutes; 1
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      Bacillus/Clostridium
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Pred. No. 5.31e-177;
38; Mismatches 44;
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                                               Signal.
                                                                                                             MUNSON S.H., TREMAINE M.T., BETLEY M.J., WEICH R.A.; "Identification and characterization of staphylococcal types G and I from Staphylococcus aureus."; Infect. Immun. 66.3337-3348(1998).
EMBL; AF064773; AAC26660.1; -.
HSSP; P01552; 1SE3.
                                                                                                                                                                                                                                                                                                                                           Staphylococcus aureus.
Staphylococcus aureus.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacteria; Firmhylococcus group; Staphylococcus.
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01-NOV-1998 (TREMBLrel. 08, Last sequence update)
01-NOV-1999 (TREMBLrel. 12, Last annotation update)
EXTRACELLULAR ENTEROTOXIN TYPE G PRECURSOR.
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085382;
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Infect. Immun. 64:1161-1165(1996).
EMBL; U48793; AAB02149.1; -.
HSSP; P34071; ISE2.
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MEDLINE; 96178602.
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REDA K.B., KAPUR V.,
RICH R.R.;
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Pred. No. 2.01e-176;
38; Mismatches 44;
POTENTIAL.
ENTEROTOXIN TYPE
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Q54696;
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Pred. No. 9.79e-106;
55; Mismatches 65;
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. No. 3.06e-107;
Mismatches 65;
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01-MAY-1997 (TrE
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J. Exp. Med. 174:1271-1274(1991).
EMBL; X61573; CAA43771.1; -.
EMBL; X61573; CAA43771.1; -.
HSSP; P34071; 1SE2
PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
   gene encoding pyrogenic exotoxin Streptococcus pyogenes.";
J. Exp. Med. 174:1271-1274(1991).
EMBL; X61556; CAA43754.1; -.
EMBL; X61557; CAA43755.1; -.
EMBL; X61560; CAA43758.1; -.
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-MGAS156, AN
MEDLINE; 92044323.
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Bacteria; Firmicutes; 1
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                                                                                                                                                                                                                                                                                                                                                             Streptococcus.
                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pyogenes.
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                                                                                                                                                                        NELSON K., SCHLIEVERT P.M., SELANDER R.K., "Characterization and clonal distribution c
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DNVRVEFKNKDLADKYKDKYVDVFGANYYYQCYFSKKTNDINSHETDKRKTCMYGGVTEH 121
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G (TrEMBLrel. )
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(TrEMBLrel. 03, Last sequence up)
(TrEMBLrel. 12, Last annotation)
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larity 46.5%;
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Pred. No. 1.32e-104;
53; Mismatches 54;
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TYPE A EXOTOXIN.
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Best Local
                                                                                                                                                                                                                                                       Streptococcus pyogenes.";
J. EXP. Med. 174:1271-1274(1991).
EMBL; X61569; CAA43767.1; -.
EMBL; X61579; CAA43766.1; -.
EMBL; X61568; CAA43766.1; -.
EMBL; X61570; CAA43768.1; -.
EMBL; X61571; CAA43769.1; -.
EMBL; X61571; 
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EMBL; X61558; CAA43757.1;
EMBL; X61559; CAA43757.1;
EMBL; X61554; CAA43752.1;
HSSP; P01552; 1SE3.
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054779 PRELIMINARY; PRT; 236 AA.
054779; Q54613; Q54736; Q54740; Q54741;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
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182 YETGYIKFI-ENENSFWYDMMPAPGDKFDQSKYLMMYNDNKMVDSKDVKI
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